

;; PRIOR FILING DATE: 1997-09-17  
;; PRIOR APPLICATION NUMBER: 60/063046  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/065027  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 60/079689  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/086478  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090689  
;; PRIOR FILING DATE: 1998-06-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 116  
;; SEQ ID NO 28  
;; LENGTH: 175  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-242-074-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 MEKIPVSALLLVALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDOLIWTQYEE 91  
DB 1 MEKIPVSALLLVALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDOLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHLLDECPHSQALKKVPFAENKEIOKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSTSNKPLMIHLLDECPHSQALKKVPFAENKEIOKLAEOQVLLNLVYETTDKHLSP 120  
QY 152 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 206  
DB 121 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 175

RESULT 5  
US-10-242-505-28  
;; Sequence 28, Application US/10242505  
;; Publication No. US20030138898A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Stephan, Jean-Phillippe  
;; APPLICANT: Watanabe, Colin  
;; APPLICANT: Wood, William  
;; APPLICANT: Zhang, Zemin  
;; APPLICANT: Fong, Sherman  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3630R1C25  
;; CURRENT APPLICATION NUMBER: US/10/242,505  
;; CURRENT FILING DATE: 2002-09-11  
;; PRIOR APPLICATION NUMBER: 10/197942  
;; PRIOR FILING DATE: 2002-07-18  
;; PRIOR APPLICATION NUMBER: 60/059114  
;; PRIOR FILING DATE: 1997-09-17  
;; PRIOR APPLICATION NUMBER: 60/063046  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/065027  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 60/079689

;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/086478  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090689  
;; PRIOR FILING DATE: 1998-06-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 116  
;; SEQ ID NO 28  
;; LENGTH: 175  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-242-505-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 MEKIPVSALLLVALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDOLIWTQYEE 91  
DB 1 MEKIPVSALLLVALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDOLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHLLDECPHSQALKKVPFAENKEIOKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSTSNKPLMIHLLDECPHSQALKKVPFAENKEIOKLAEOQVLLNLVYETTDKHLSP 120  
QY 152 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 206  
DB 121 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 175

RESULT 6  
US-10-242-574-28  
;; Sequence 28, Application US/10242574  
;; Publication No. US20030138899A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Stephan, Jean-Phillippe  
;; APPLICANT: Watanabe, Colin  
;; APPLICANT: Wood, William  
;; APPLICANT: Zhang, Zemin  
;; APPLICANT: Fong, Sherman  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3630R1C20  
;; CURRENT APPLICATION NUMBER: US/10/242,574  
;; CURRENT FILING DATE: 2002-09-11  
;; PRIOR APPLICATION NUMBER: 10/197942  
;; PRIOR FILING DATE: 2002-07-18  
;; PRIOR APPLICATION NUMBER: 60/059114  
;; PRIOR FILING DATE: 1997-09-17  
;; PRIOR APPLICATION NUMBER: 60/063046  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/065027  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 60/079689  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/086478  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/089801

; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-242-574-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred.No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 MEKIPVSFAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQTYEE 91  
Db 1 MEKIPVSFAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQTYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEQFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEQFVLLNLVYETTDKHLSP 120  
QY 152 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206  
Db 121 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

## RESULT 7

US-10-243-261-28  
; Sequence 28, Application US/10243261  
; Publication No. US20030138900A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C56  
; CURRENT APPLICATION NUMBER: US/10/243,261  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-243-261-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred.No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 MEKIPVSFAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQTYEE 91  
Db 1 MEKIPVSFAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQTYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEQFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEQFVLLNLVYETTDKHLSP 120  
QY 152 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206  
Db 121 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

## RESULT 8

US-10-243-282-28  
; Sequence 28, Application US/10243282  
; Publication No. US20030138901A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C50  
; CURRENT APPLICATION NUMBER: US/10/243,282  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-243-282-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQYEE 91  
DB 1 MEKIPVSAFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQYEE 60

QY 92 ALYKSKTSNKPMLIIHLLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSKTSNKPMLIIHLLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 120

QY 152 DQGVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 206  
DB 121 DQGVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 175

RESULT 10  
US-10-243-431-28  
; Sequence 28, Application US/10243431  
; Publication No. US20030138903A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C37  
; CURRENT APPLICATION NUMBER: US/10/243,431  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-243-431-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQYEE 91  
DB 1 MEKIPVSAFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQYEE 60

QY 92 ALYKSKTSNKPMLIIHLLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSKTSNKPMLIIHLLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 120

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQYEE 91  
DB 1 MEKIPVSAFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQYEE 60

QY 92 ALYKSKTSNKPMLIIHLLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSKTSNKPMLIIHLLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 120

QY 152 DQGVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 206  
DB 121 DQGVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 175

RESULT 9  
US-10-243-402-28  
; Sequence 28, Application US/10243402  
; Publication No. US20030138902A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C39  
; CURRENT APPLICATION NUMBER: US/10/243,402  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-243-402-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQYEE 91  
DB 1 MEKIPVSAFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQYEE 60

QY 92 ALYKSKTSNKPMLIIHLLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSKTSNKPMLIIHLLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 120

QY 152 DQYVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDNNMKALKLKTTEL 206  
Db 121 DQYVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDNNMKALKLKTTEL 175

## RESULT 11

US-10-245-164-28  
; Sequence 28, Application US/10245164  
; Publication No. US20030138904A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C76  
; CURRENT APPLICATION NUMBER: US/10/245,164  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-245-164-28  
Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 91  
Db 1 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLNLVYETTDKHLSP 120  
QY 152 DQYVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDNNMKALKLKTTEL 206  
Db 121 DQYVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDNNMKALKLKTTEL 175

## RESULT 12

US-09-903-190-106  
; Sequence 106, Application US/09903190  
; Publication No. US20030162176A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET 021A  
; CURRENT APPLICATION NUMBER: US/09/903,190  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: US/09/247,155A  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 106  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -20...-1

US-09-903-190-106  
Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 91  
Db 1 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLNLVYETTDKHLSP 120  
QY 152 DQYVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDNNMKALKLKTTEL 206  
Db 121 DQYVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDNNMKALKLKTTEL 175

## RESULT 13

US-10-244-972-28  
; Sequence 28, Application US/10244972  
; Publication No. US20030170809A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C75  
; CURRENT APPLICATION NUMBER: US/10/244, 972  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942

US-10-244-972-28  
Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 91  
Db 1 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLNLVYETTDKHLSP 120  
QY 152 DQYVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDNNMKALKLKTTEL 206  
Db 121 DQYVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDNNMKALKLKTTEL 175

```
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/084678
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/106932
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119342
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/123957
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123972
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/127372
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/131271
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/133459
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/135725
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/135729
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138385
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/140653
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144732
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/144790
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145228
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146843
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/148188
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/148513
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/149327
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149395
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/150114
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/151700
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/151734
; PRIOR FILING DATE: 1999-08-31

Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSALLLVALSYLTARDTTVKCAKDKTDSRPKLPQTLSRGWDQLIWTQYEE 91
Db 1 MEKIPVSALLLVALSYLTARDTTVKCAKDKTDSRPKLPQTLSRGWDQLIWTQYEE 60

Qy 92 ALYKSTSNKPLMIHHLDECPHSQALKKVPFAENKIQKLAEQFVLLNLVYETTDKHLSP 151
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVPFAENKIQKLAEQFVLLNLVYETTDKHLSP 120

Qy 152 DGQVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLLDNNKKALKLLKTEL 206
Db 121 DGQVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLLDNNKKALKLLKTEL 175

RESULT 14
US-10-197-942-28
; Sequence 28, Application US/10197942
; Publication No. US20030175882A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C1(US)
; CURRENT APPLICATION NUMBER: US/10/197,942
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
```

PRIOR APPLICATION NUMBER: 60/162506  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 60/170262  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/177118  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: 60/179851  
PRIOR FILING DATE: 2000-02-02  
PRIOR APPLICATION NUMBER: 60/180921  
PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 60/187202  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/198587  
PRIOR FILING DATE: 2000-04-18  
PRIOR APPLICATION NUMBER: 60/199614  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 60/206330  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/206368  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/209832  
PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: 60/218371  
PRIOR FILING DATE: 2000-07-13  
PRIOR APPLICATION NUMBER: 60/222695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/229896  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/230621  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/232887  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/235147  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/261878  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 60/261910  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/261939  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/262150  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/264395  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/266421  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 60/267623  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/274399  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/280982  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/282129  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/282199  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/290589  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: 09/180997  
PRIOR FILING DATE: 1998-11-19  
PRIOR APPLICATION NUMBER: 09/267213  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 09/380137  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/403297  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: 09/423741  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: 09/709238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/802706

PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 09/872035  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/924419  
PRIOR FILING DATE: 2001-08-06  
PRIOR APPLICATION NUMBER: 09/927796  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 09/941992  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: 09/946374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 10/001054  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 10/081056  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 10/119480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: PCT/US98/18824  
PRIOR FILING DATE: 1998-09-10

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLVLSYTLARDTTVKPGAKKDTKOSRPLQTLNRGWDQLIWTQYEE 91  
DB 1 MEKIPVSAFLLVLSYTLARDTTVKPGAKKDTKOSRPLQTLNRGWDQLIWTQYEE 60

QY 92 ALYKSKTSNKPLMIHHLDECPSHQSALKKVFAENKEIQKLAEOFLVLLNLYVETTDKHLSP 151  
DB 61 ALYKSKTSNKPLMIHHLDECPSHQSALKKVFAENKEIQKLAEOFLVLLNLYVETTDKHLSP 120

QY 152 DGQYVPRIMFVDPSTLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206  
DB 121 DGQYVPRIMFVDPSTLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

RESULT 15  
US-10-238-196-28  
Sequence 28, Application US/10238196  
Publication No. US20030186372A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C8  
CURRENT APPLICATION NUMBER: US/10/238,196  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24

```

; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-196-28

```

```

Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSFLLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDOLIWTQYEE 91
Db 1 MEKIPVSFLLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDOLIWTQYEE 60

Qy 92 ALYKSTSNKPLMIHHLDCEPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETDDKHLSP 151
Db 61 ALYKSTSNKPLMIHHLDCEPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETDDKHLSP 120

Qy 152 DGQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 206
Db 121 DGQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 175

```

Search completed: November 26, 2003, 16:01:22  
Job time : 32 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2003, 15:53:44 ; Search time 21 Seconds  
(without alignments)  
415.049 Million cell updates/sec

Title: US-09-674-266A-181  
Perfect score: 103  
Sequence: 1 RLSCAGTSGSPHPSRLT.....DTALLDNMKALKLKTLE 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	899	84.6	175	3	US-08-916-576B-2
2	899	84.6	175	4	US-09-247-155-106
3	609.5	57.3	170	3	US-08-916-576B-8
4	605	56.9	131	4	US-09-247-155-174
5	555	52.2	166	3	US-08-916-576B-6
6	448	42.1	183	3	US-08-916-576B-7
7	222	20.9	172	3	US-08-916-576B-4
8	88.5	8.3	118	4	US-09-198-452A-1234
9	81.5	7.7	901	2	US-08-884-681-5
10	81.5	7.7	901	3	US-09-258-643-5
11	81.5	7.7	968	3	US-08-560-005-7
12	81.5	7.7	968	3	US-09-418-540-7
13	81.5	7.7	968	4	US-09-969-528-7
14	79	7.4	166	4	US-09-198-452A-998
15	78	7.3	129	4	US-09-534-638-5
16	78	7.3	453	3	US-09-013-881-5
17	78	7.3	453	4	US-09-612-473-5
18	78	7.3	1160	5	PCT-US92-05401-4
19	77	7.2	652	2	US-08-313-185-53
20	77	7.2	652	2	US-08-459-499-17
21	77	7.2	652	3	US-09-082-614A-53
22	77	7.2	1049	4	US-09-107-532A-5966
23	74.5	7.0	2321	4	US-09-230-652-2
24	74	7.0	264	3	US-09-053-197A-8
25	74	7.0	264	4	US-09-085-761A-8
26	73.5	6.9	1049	4	US-09-252-991A-17298
27	73	6.9	1067	4	US-09-107-532A-5148

28	71.5	6.7	352	3	US-08-921-887-52	Sequence 52, Appl
29	71.5	6.7	382	4	US-09-134-001C-3765	Sequence 3765, Ap
30	71.5	6.7	508	4	US-09-252-991A-32765	Sequence 32765, A
31	71.5	6.7	588	4	US-09-328-352-7994	Sequence 7994, Ap
32	71.5	6.7	698	4	US-09-107-532A-5685	Sequence 5685, Ap
33	71	6.7	529	3	US-08-821-984-6	Sequence 6, Appli
34	71	6.7	529	3	US-08-821-984-8	Sequence 8, Appli
35	71	6.7	529	3	US-09-329-749-6	Sequence 6, Appli
36	71	6.7	529	3	US-09-329-749-8	Sequence 8, Appli
37	71	6.7	529	4	US-09-502-264-6	Sequence 6, Appli
38	71	6.7	529	4	US-09-502-264-8	Sequence 8, Appli
39	70.5	6.6	481	1	US-08-186-811-2	Sequence 2, Appli
40	70.5	6.6	481	1	US-08-311-611A-98	Sequence 98, Appl
41	70.5	6.6	481	1	US-08-372-783-98	Sequence 98, Appl
42	70.5	6.6	481	1	US-08-372-105-98	Sequence 98, Appl
43	70.5	6.6	481	1	US-08-306-473A-98	Sequence 98, Appl
44	70.5	6.6	481	1	US-08-261-660A-4	Sequence 4, Appli
45	70.5	6.6	481	1	US-08-209-762-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1  
US-08-916-576B-2  
; Sequence 2, Application US/08916576B  
; Patent No. 6171816  
; GENERAL INFORMATION:  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: DILLON, PATRICK J.  
; APPLICANT: EBNER, REINHARD  
; APPLICANT: ENDRESS, GREGORY A.  
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,576B  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,347  
; FILING DATE: 23-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0500001  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-916-576B-2

Query Match 84.6%; Score 899; DB 3; Length 175;  
Best Local Similarity 100.0%; Pred. No. 1.6e-95;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSALLVALSYTLARDTTVRPGAKKDTKDSRKLPTQLSRGWGDLWTQTYEE 91

Db 1 MEKIPVSFALLVALSYTLARDTTVPAGAKDTKDSRPKLPQTLSRGWGDLWTQTYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPSHQALKKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPSHQALKKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 120  
QY 152 DGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206  
Db 121 DGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

RESULT 2

US-09-247-155-106  
; Sequence 106, Application US/09247155A  
; Patent No. 6312922  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; CURRENT FILING DATE: 1999-02-09  
; EARLIER APPLICATION NUMBER: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER APPLICATION NUMBER: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/099,273  
; EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 106  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -20..-1  
US-09-247-155-106

Query Match 84.6%; Score 899; DB 4; Length 175;  
Best Local Similarity 100.0%; Pred. No. 1.6e-95;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFALLVALSYTLARDTTVPAGAKDTKDSRPKLPQTLSRGWGDLWTQTYEE 91  
Db 1 MEKIPVSFALLVALSYTLARDTTVPAGAKDTKDSRPKLPQTLSRGWGDLWTQTYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPSHQALKKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPSHQALKKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 120  
QY 152 DGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206  
Db 121 DGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

RESULT 3

US-08-916-576B-8  
; Sequence 8, Application US/08916576B  
; Patent No. 6171816  
; GENERAL INFORMATION:  
; APPLICANT: YU GUO-LIANG  
; APPLICANT: DILLON, PATRICK J.  
; APPLICANT: EBNER, REINHARD  
; APPLICANT: ENDRSS, GREGORY A.  
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,576B  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,347  
; FILING DATE: 23-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0500001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-916-576B-8

Query Match 57.3%; Score 609.5; DB 3; Length 170;  
Best Local Similarity 71.3%; Pred. No. 3.2e-62;  
Matches 122; Conservative 14; Mismatches 26; Indels 9; Gaps 2;  
QY 37 VSAFLLVALSYTLARDTTVPAGAKDTKDSRP-KLPQTLSRGWGDLWTQTYEALYK 95  
Db 7 LGACLLVALSYXLA-----XXXKGDXRPKPGQTLSRGWGDXIXWVQTYEGLKX 58  
QY 96 SKTSNKPMLIIHHLDECPSHQALKKVFAENKEIQKLAQFVLLNLVYETTDKHLSPDGQY 155  
Db 59 AXSNKPLMVIHLEDCPSYQALKKVFAENKEIQKLAQFVLLNLVYETTDENLSPDGQY 118  
QY 156 VPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206  
Db 119 VPRIMFVPSLTVRADITGRYSNRLYAYEPDXPLIXNNKKALKLLKTEL 169

RESULT 4

US-09-247-155-174  
; Sequence 174, Application US/09247155A  
; Patent No. 6312922  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; CURRENT FILING DATE: 1999-02-09  
; EARLIER APPLICATION NUMBER: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER APPLICATION NUMBER: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/099,273  
; EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 174

LENGTH: 131

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: -20...-1

FEATURE: UNSURE

NAME/KEY: 40,41,43,60,70,76,82,86,105,107

LOCATION: 40,41,43,60,70,76,82,86,105,107

OTHER INFORMATION: Xaa = any one of the twenty amino acids

US-09-247-155-174

Query Match

Best Local Similarity 56.9%; Score 605; DB 4; Length 131;

Mismatches 9; Indels 0; Gaps 0;

Matches 117; Conservative 9; Indels 0; Gaps 0;

Qy 32 MEKIPVSAPLLVALSYTLARDTTVKCAKDTKDSRPKLPQTLSRGWDQDLWTOTYEE 91

Db 1 MEKIPVSAPLLVALSYTLARDTTVKCAKDTKDSRPKLPQTLSRGWDQDLWTOTYEX 60

Qy 92 ALYKSKTSNKPLMIHHLDECPSQALKKVFPAENKEIOKLAEQFVLLNLVYETTDKHLSP 151

Db 61 XLKSKTSNKPLMIHHLDECPSQALKKVFPAENKXIOKLAEQFVLLNLVYETTDKHLSP 120

Qy 152 DGQYVP 157

Db 121 DGQYXP 126

RESULT 5

US-08-916-576B-6

Sequence 6, Application US/08916576B

Patent No. 6171816

GENERAL INFORMATION:

APPLICANT: YU, GUO-LIANG

APPLICANT: DILLON, PATRICK J.

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

Query Match

Best Local Similarity 52.2%; Score 555; DB 3; Length 166;

Mismatches 28; Conservative 19; Indels 12; Gaps 4;

Matches 108; Conservative 19; Indels 12; Gaps 4;

Qy 41 LLLVALSYTLARDTTVKGAKKDTKDSRPKLPQTLSRGWDQDLWTOTYEEALYKSKTSN 100

Db 11 LLLVTSSNLA--IAIK-----KEKRP--PQTLSRGWDQDLWTOTYEEGLFYAQS 59

Qy 101 KPLMIHHLDECPSQALKKVFPAENKEIOKLAE--QFVLLNLVYETTDKHLSPDQGYVPRI 159

Db 60 KPLMIHHLDECPSQALKKVFPAENKEIOKLAE--QFVLLNLVYETTDKHLSPDQGYVPRI 119

Qy 160 MFVDPSTLVRADITGRYSNRLYAYEPADTALLDNMKKALKLKLTEL 206

Db 120 MFVDPSTLVRADITGRYSNRLYAYEPADTALLDNMKKALKLKLTEL 166

RESULT 6

US-08-916-576B-7

Sequence 7, Application US/08916576B

Patent No. 6171816

GENERAL INFORMATION:

APPLICANT: YU, GUO-LIANG

APPLICANT: DILLON, PATRICK J.

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

APPLICANT: EBNR, REINHARD

Query Match

Best Local Similarity 42.1%; Score 448; DB 3; Length 183;

Mismatches 29; Conservative 29; Indels 10; Gaps 3;

Matches 88; Conservative 29; Indels 10; Gaps 3;

Qy 39 AFLLLVALSYTLARDTTVKP---GAKDXTKDSRPKLP-----QTLSRGWDQDLWTOTY 89

Db 6 SLVCLVLLCSALGEAVLKPKQAGTTDTKTDOEPAPIKTKGLKTLDRGWSIEWQTY 65

Qy 90 EEALYKSKTSNKPLMIHHLDECPSQALKKVFPAENKEIOKLAE--QFVLLNLVYETTDKHL 148

```
Db 66 EBLAKARENKPMWHLHLEDCPSIALKKAFAVADRMQAOKLAQEDFIMNLVHPVADEN 125
QY 149 LSPDGOYVPRIMVDFSLTVRADITGRYSNRLYAYEPADTALLDNKKALKLLKTEL 206
Db 126 QSPDGHVPRVIFDPSLTVRSDLKGRYKMYAYDADDIPELITNKKAKSFLKTEL 183

RESULT 7
US-08-916-576B-4
; Sequence 4, Application US/08916576B
; Patent No. 6171816
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: EBNER, REINHARD
; APPLICANT: ENDRESS, GREGORY A.
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,576B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,347
; FILING DATE: 23-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0500001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-576B-4

Query Match 20.9%; Score 222; DB 3; Length 172;
Best Local Similarity 34.2%; Pred. No. 1.4e-17;
Matches 54; Conservative 26; Mismatches 56; Indels 22; Gaps 3;

QY 66 DSRPKLPQT-----LSRGWGDQLIWTQYEEALYKSKTSKNKPLMII 106
Db 2 ETRPRGATCLGFSFLLLVSSDGHNLGKFGDHIHW-RTLEDGKKEAAASGLPLMVI 60

QY 107 HHLDECHPSOALKKVFPAENKEIQKLAQFVLLNL--VYETTDKHLSPDGOYVPRIMVDP 164
Db 61 IHKSWCGACKALKPKFAESTEISELSHNFVMVNLDEEPEKDEDFSPDGGYIIRILFLDP 120

QY 165 SLTVRADITGRYSNRLYAYEPADTALLDNKKALKLL 202
Db 121 SGKVHPEIINENGPNPSYKYFVVSABQVQGMKEAQERL 158

RESULT 8
US-09-198-452A-1234
; Sequence 1234, Application US/09198452A
```

```
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev.
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1234
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1234

Query Match 8.3%; Score 88.5; DB 4; Length 118;
Best Local Similarity 24.6%; Pred. No. 0.018;
Matches 33; Conservative 29; Mismatches 45; Indels 27; Gaps 5;

QY 29 RVAMEKIPVSAFLLLVALSYYTLARDTTVPKAKKDTKDSRPKLQTLSRGWGDQLIWTQT 88
Db 9 RCLSKQLKVLATLL---LSLSL-----PTLEAENRDS-----DSIVVHLD 46

QY 89 YEEALYKSKTSKNKPLMI IHHLDEC--PHSQALKKVFPAENKEIQKLAQFVLLNLVYETTD 146
Db 47 YQALQKSKAEALPLLVIFSGSDWNGPCMKIRKEVLESPEFIKRVQGVCEVEYL--- 103

QY 147 KHLSPDGOYVPRIM 160
Db 104 KHRPQLKTFVSKIL 117

RESULT 9
US-08-884-681-5
; Sequence 5, Application US/08884681
; Patent No. 5955338
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,681
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0334 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 901 amino acids
; TYPE: amino acid
```

STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1420920  
US-08-884-681-5

Query Match 7.7%; Score 81.5; DB 2; Length 901;  
Best Local Similarity 23.7%; Pred. No. 2.3;  
Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;  
Qy 55 TVKPGAKKOTKDSRPK--LPQTLRGWGQDLWTQTYEEAL-YKS-----KTS-NKPLMII 106  
Db 476 TYKYDSTDRWDSSGKCRVP-----AWCDRLWRGTNVNQLYRSHMELKTSDHKPVSA 530  
Qy 107 HHL-----DECPHQAQKVKFAENKEIQKLAEE-----QFVLLNLVYETTDK-- 147  
Db 531 FHIGVKVUDE-----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFNKFRLOQK 586  
Qy 148 -HLSPDGQ-----YVPRIM-----FVDPSTVTRADITGRYSNRLYAYE 184  
Db 587 FQISNNGQVPCHFSPFKPLNDSQYCKPWLRAEPFEGYLEPNETV--DIS-----LDVYV 638  
Qy 185 PADTALLDN 194  
Db 639 SKDSVTILNS 648

## RESULT 10

US-09-258-643-5  
; Sequence 5, Application US/09258643  
; Patent No. 6277373  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/258,643  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/884,681  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0334 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 901 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1420920

## US-09-258-643-5

Query Match 7.7%; Score 81.5; DB 3; Length 901;  
Best Local Similarity 23.7%; Pred. No. 2.3;  
Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;  
Qy 55 TVKPGAKKOTKDSRPK--LPQTLRGWGQDLWTQTYEEAL-YKS-----KTS-NKPLMII 106  
Db 476 TYKYDSTDRWDSSGKCRVP-----AWCDRLWRGTNVNQLYRSHMELKTSDHKPVSA 530  
Qy 107 HHL-----DECPHQAQKVKFAENKEIQKLAEE-----QFVLLNLVYETTDK-- 147  
Db 531 FHIGVKVUDE-----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFNKFRLOQK 586  
Qy 148 -HLSPDGQ-----YVPRIM-----FVDPSTVTRADITGRYSNRLYAYE 184  
Db 587 FQISNNGQVPCHFSPFKPLNDSQYCKPWLRAEPFEGYLEPNETV--DIS-----LDVYV 638  
Qy 185 PADTALLDN 194  
Db 639 SKDSVTILNS 648

## RESULT 11

US-08-560-005-7  
; Sequence 7, Application US/08560005  
; Patent No. 6001354  
; GENERAL INFORMATION:  
; APPLICANT: Pot, David A.  
; APPLICANT: Williams, Lewis T.  
; APPLICANT: Jefferson, Anne Bennett  
; APPLICANT: Majerus, Philip W.  
; TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and Nucleic  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/560,005  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 2307K-0624000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 968 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..968  
; OTHER INFORMATION: /note= "ocr1"  
; US-08-560-005-7

Query Match 7.7%; Score 81.5; DB 3; Length 968;  
Best Local Similarity 23.7%; Pred. No. 2.6;  
Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;

Qy	55	TVKPGAKDITKDSRPK--LPOTLSRGWGDLITQTVEEAL--YKS-----KTS--NKPLMLI 106
Db	551	TVKYDSKTDKRWDSGKCRVP-----AMCDRIILMRGTNVNQLNVRSHMLLXATSDHKPVSAL 605
Qy	107	HHL-----DECPSQALKKVFPAENKEIQKLAE-----QFVLLNLVVEITTDK-- 147
Db	606	PHIGVKWVDE----RYYRKVPEDSVRINDRMENDFLPSLSRRFEFVFNKVRQLOQKG 661
Qy	148	-HLSPDGQ-----YVPRIM-----FVDPSLTVRAIDITGRYSNRLYAYE 184
Db	662	FOISNNGQVPCHFSFIPKLNDSQYCKPWLRAEPPEGYLENETV--DIS-----LDVYV 713
Qy	185	PADTALLDN 194
Db	714	SKDSVTILNS 723

```

RESULT 12
US-09-418-540-7
; Sequence 7, Application US/09418540
; Patent No. 6296848
; GENERAL INFORMATION:
; APPLICANT: Pot, David A.
; APPLICANT: Williams, Lewis T.
; APPLICANT: Jefferson, Anne Bennett
; APPLICANT: Majerus, Philip W.
; TITLE OF INVENTION: No. 6296848el Grb2 Associating Protein and Nucleic
; TITLE OF INVENTION: Acids Encoding Therefor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/418,540
; FILING DATE: 14-OCT-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/560,005
; FILING DATE: 17-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-0624000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 968 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..968
; OTHER INFORMATION: /note= "ocr1"
US-09-418-540-7

```

[illegible]

Db 551 TYKDSKTRDRWSSGKCRVP-----AWCDRIILWRGNNVNLNRYRSHMLLKTSDHKFVSAL 605  
QY 107 HHL-----DECPHSAKVKVFAENKEIQKLA-----QFVLNLVYETTK-- 147  
Db 606 FHIGVWVDE-----RRYKVFEDSVIRMDRMENDFLPSLELSRREFVFNKFRQLQKQK 661  
QY 148 -HLSPDGQ-----YVPRIM-----FVDPSTVTRADITGRYSNRLYAYE 184  
Db 662 FOISNNGQVPCHFSPITPLNDSQYCKPMLRABPFEGYLEPNETV--DIS-----LDVVV 713  
QY 185 PADTALLLN 194  
Db 714 SKDSVTILNS 723

RESULT 14  
US-09-198-452A-998  
; Sequence 998, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 998  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-998

Query Match 7.4%; Score 79; DB 4; Length 166;  
Best Local Similarity 24.2%; Pred. No. 0.37;  
Matches 43; Conservative 27; Mismatches 70; Indels 38; Gaps 9;  
QY 40 FLLVALSVTLARDTTVPKAKKTDKSRPKLPQTLSRGWGDLIWTQTYEALYKSKTS 99  
Db 10 FCLSAIDFTLLCCT--KTCFWRNLQOTRPIAANLQ-----W-ESYAEALEHSKQD 58  
QY 100 NKPL-MIIHLDDECPHSAKVKVFAENKEIQKLAEQFVLLNLV-----YETTDK 147  
Db 59 HKPICLFTGSDWCWCIKMQDQILQSSEFKHFAG--VHLHMEVDVFPQKXHQPEQRQK 116  
QY 148 HLSPDGQY-----VPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNKKALKL 201  
Db 117 NOELKAQYKVTGFPPELVFIDAE-----GKQLARM-GFEPGGGAAYVSVKYSALKL 165

RESULT 15  
US-09-534-638-5  
; Sequence 5, Application US/09534638  
; Patent No. 6320038  
; GENERAL INFORMATION:  
; APPLICANT: Panula, Pertti A.J.  
; APPLICANT: Brandt, Annika  
; APPLICANT: Westerland, Johanna  
; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof  
; TITLE OF INVENTION: for therapy and diagnosis  
; FILE REFERENCE: 2530-104  
; CURRENT APPLICATION NUMBER: US/09/534,638  
; CURRENT FILING DATE: 2000-03-27  
; EARLIER APPLICATION NUMBER: 09/365755  
; EARLIER FILING DATE: 1999-08-03  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-534-638-5

Query Match 7.3%; Score 78; DB 4; Length 129;  
Best Local Similarity 22.9%; Pred. No. 0.34;  
Matches 16; Conservative 14; Mismatches 40; Indels 0; Gaps 0;  
QY 44 VALSVTLARDTTVPKAKKTDKSRPKLPQTLSRGWGDLIWTQTYEALYKSKTSNKPL 103  
Db 3 IALFYILLTCSNTSPSSRNSTQSGSPQAPVVDSDRWEDTVLWAVLLQKCLLSFPSSQFSM 62  
QY 104 MIIHLDDECP 113  
Db 63 TPVSRLSOSP 72

Search completed: November 26, 2003, 15:56:59  
Job time : 22 secs

**THIS PAGE BLANK (USPTO)  
BEST AVAILABLE COPY**

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 30, 2003, 02:24:26 ; Search time 64 Seconds  
(without alignments)  
1420.702 Million cell updates/sec

Title: US-09-674-266A-181  
Perfect score: 1063  
Sequence: 1 RUSCAGTUGSGPHSPRRLLT.....DTALLDNMKKALKLLKTEL 206

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool/US09674266/runat\_26112003\_152749\_15781/app\_query.fasta\_1.391  
-DB=Issued\_Patents NA -QFMT=fastap -SUFFIX=sn1 -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09674266 @CGN 1.1 56 @runat\_26112003\_152749\_15781 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT\_DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991	93.2	875	3 US-08-916-576B-1	Sequence 1, Appli
2	961	90.4	1689	4 US-09-247-155-61	Sequence 61, Appl
3	914	86.0	940	4 US-09-247-155-149	Sequence 149, App
4	856.5	80.6	793	3 US-09-040-984-78	Sequence 78, Appl
5	856.5	80.6	793	4 US-09-123-912-78	Sequence 78, Appl
6	856.5	80.6	793	4 US-09-643-597-78	Sequence 78, Appl
7	856.5	80.6	793	4 US-09-480-884A-78	Sequence 78, Appl
8	856.5	80.6	793	4 US-09-542-615A-78	Sequence 78, Appl
9	856.5	80.6	793	4 US-09-606-421B-78	Sequence 78, Appl
10	683	64.3	401	3 US-09-221-298-32	Sequence 32, Appl
11	642	60.4	386	3 US-08-916-576B-35	Sequence 35, Appl
12	631	59.4	404	4 US-09-643-597-282	Sequence 282, App

13	631	59.4	404	4	US-09-480-884A-282	Sequence 282, App
14	631	59.4	404	4	US-09-542-615A-282	Sequence 282, App
15	631	59.4	404	4	US-09-606-421B-282	Sequence 282, App
16	555	52.2	732	3	US-08-916-576B-5	Sequence 5, Appl
17	547	51.5	321	4	US-09-389-681-218	Sequence 218, App
18	547	51.5	321	4	US-09-620-405B-218	Sequence 218, App
19	547	51.5	321	4	US-09-339-338-218	Sequence 218, App
20	547	51.5	321	4	US-09-433-826B-218	Sequence 218, App
21	547	51.5	321	4	US-09-604-287A-218	Sequence 218, App
22	487.5	45.9	373	3	US-08-916-576B-36	Sequence 36, Appl
23	458.5	43.1	489	3	US-08-916-576B-9	Sequence 9, Appl
24	384	36.1	235	4	US-09-702-705-410	Sequence 410, App
25	384	36.1	235	4	US-09-736-457-410	Sequence 410, App
26	376.5	35.4	506	3	US-08-916-576B-10	Sequence 10, Appl
27	266	25.0	198	4	US-09-702-705-1183	Sequence 1183, Ap
28	266	25.0	198	4	US-09-702-705-1576	Sequence 1576, Ap
29	266	25.0	198	4	US-09-736-457-1183	Sequence 1183, Ap
30	266	25.0	198	4	US-09-736-457-1576	Sequence 1576, Ap
31	253	23.8	158	3	US-08-916-576B-37	Sequence 37, Appl
32	252	23.7	159	4	US-09-030-607-209	Sequence 209, App
33	252	23.7	159	4	US-09-439-311-209	Sequence 209, App
34	252	23.7	159	4	US-09-352-616A-209	Sequence 209, App
35	252	23.7	159	4	US-09-232-149A-209	Sequence 209, App
36	237	22.3	171	4	US-09-389-681-412	Sequence 412, App
37	237	22.3	171	4	US-09-620-405B-412	Sequence 412, App
38	237	22.3	171	4	US-09-433-826B-412	Sequence 412, App
39	237	22.3	171	4	US-09-604-287A-412	Sequence 412, App
40	222	20.9	1423	3	US-08-916-576B-3	Sequence 3, Appl
41	183.5	17.3	136	3	US-08-916-576B-38	Sequence 38, Appl
42	158	14.9	302	3	US-08-916-576B-19	Sequence 19, Appl
43	147.5	13.9	310	3	US-08-916-576B-41	Sequence 41, Appl
44	129	12.1	311	3	US-08-916-576B-40	Sequence 40, Appl
45	104	9.8	329	3	US-08-916-576B-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-916-576B-1  
; Sequence 1, Application US/08916576B  
; Patent No. 6171816  
; GENERAL INFORMATION:  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: DILLON, PATRICK J.  
; APPLICANT: EBER, REINHARD  
; APPLICANT: ENDRESS, GREGORY A.  
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,576B  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,347  
; FILING DATE: 23-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0500001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600

GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; EARLIER FILING DATE: 1999-02-09  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 61  
; LENGTH: 1689  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 51..575  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 51..110  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 11.2  
; OTHER INFORMATION: seq AFLILVALSYTLA/RD  
; FEATURE:  
; NAME/KEY: polyA signal  
; LOCATION: 1653..1658  
; FEATURE:  
; NAME/KEY: polyA site  
; LOCATION: 1674..1689  
; US-09-247-155-61

TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 875 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 71..595  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 131..595  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 71..130  
; US-08-916-576B-1

Alignment Scores:  
Pred. No.: 6.88e-117 Length: 875  
Score: 991.00 Matches: 193  
Percent Similarity: 99.48% Conservative: 0  
Best Local Similarity: 99.48% Mismatches: 1  
Query Match: 93.23% Indels: 0  
DB: 3 Gaps: 0

US-09-674-266A-181 (1-206) x US-08-916-576B-1 (1-875)  
Qy 13 ProHisProSerArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMet 32  
Db 14 CCGATTCTCCAGCGCGGCTCACACAGCGAGGTGGGTGAGGAATCCAGAGTGGCCATG 73  
Qy 33 GluLysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArg 52  
Db 74 GAGAAATTCAGTGTGAGCATCTTGTCTTGTGGCCCTCTCTACACTCTGGCCAGA 133  
Qy 53 AspThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuPro 72  
Db 134 GATACACAGTCAACCTGGAGCCAAAGGACACAAAGGACTCTCGACCCCAATGGCC 193  
Qy 73 GlnThrLeuSerArgGlyTrpGlyAspGlnLeuLeuTrpThrGlnThrTyrGluGluAla 92  
Db 194 CAGACCCCTCCAGAGGTGGGTGACCAACTCATCTGGACTCAGACATATGAGAGCT 253  
Qy 93 LeuTyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLysLeuAspGluCys 112  
Db 254 CTATATAATCCAAAGCAAGCAACAAACCTTGTGATGATTTATTCATCATCTGGATGATGC 313  
Qy 113 ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluLeuGlnLysLeuAla 132  
Db 314 CCACACAGTCAAGCTTTAAAGAAAGTGTGTGCTGAAATAAAGAAATCCAGAAATGGCA 373  
Qy 133 GluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLysSerProAsp 152  
Db 374 GAGCAGTGTGCTCTCAATCGGTTTATGAACAACTGACAAACACCTTCTCTCTGAT 433  
Qy 153 GlyGlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIle 172  
Db 434 GGCAGTATGTCCTCCAGGATATGTTGTGACCCATCTCTGACAGTTAGAGCCGATATC 493  
Qy 173 ThrGlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeu 192  
Db 494 ACTGGAAGATATTCAAATCGTCTATGCTTACGAACCTGCAACCTGACATACAGTCTGTGCTT 553  
Qy 193 AspAsnMetLysLysAlaLeuLysLeuLeuLysThrGluLeu 206  
Db 554 GACAACTGAAGAAGCTCTCAAGTTGCTGAAGACTGAAATG 595

Alignment Scores:  
Pred. No.: 1.3e-112 Length: 1689  
Score: 961.00 Matches: 189  
Percent Similarity: 96.92% Conservative: 0  
Best Local Similarity: 96.92% Mismatches: 0  
Query Match: 90.40% Indels: 6  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-247-155-61 (1-1689)  
Qy 12 GlyProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAla 31  
Db 9 GACCCGATCTCTAGCGCGGACTCACACAGGC-----AGAGTTGCC 50  
Qy 32 MetGluLysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAla 51  
Db 51 ATGGAGAAATTCAGTGTGCGATTCCTTGTGCGCTCTCTCTACACTCTGGCC 110  
Qy 52 ArgAspThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeu 71  
Db 111 AGATATCCACAGTCAAACTGGAGCCAAAGGACACAAAGGACTCTCGACCCAAACTG 170  
Qy 72 ProGlnThrLeuSerArgGlyTrpGlyAspGlnLeuLeuTrpThrGlnThrTyrGluGlu 91  
Db 171 CCCACAGCCCTCTCCAGAGGTTGGGTGACCAACTCATCTCGGACTCAGACATATGAAGAA 230  
Qy 92 AlaLeuTyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLysLeuAspGlu 111  
Db 231 GCTCTATATAAATCCAAGCAAGCAACAAACCTTGTATGATTATTCTATCATCTGGATGAG 290  
Qy 112 CysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluLeuGlnLysLeu 131  
Db 291 TGCCCAACAGTCAAGCTTTAAGAAAGTGTGTCTGAAATAAAGAAATCCAGAAATTTG 350

Qy 132 AlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerPro 151  
Db 351 GCAGAGCAGTTTGTCTCTCTCAATCTGTTTATGAAACCACTGACAAACACCTTTCTCT 410  
Qy 152 AspGlyGlnTyrValProArgGlyMetPheValAspProSerLeuThrValArgAlaAsp 171  
Db 411 GATGGCAGATATGTCCTCAGATATGTTGTTGACCCATCTCTGACAGTTAGAGCCGAT 470  
Qy 172 IleThrGlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeu 191  
Db 471 ATCACTGGAAGATATCAATCGTCTCTATGCTTACGACCTGACAGATCAGCTCTGTTG 530  
Qy 192 LeuAspAsnMetLysLysAlaLeuLysLeuLeuLysThrGluLeu 206  
Db 531 CTTGACACATGAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG 575

## RESULT 3

US-09-247-155-149  
; Sequence 149, Application US/09247155A  
; Patent No. 6312922

## ; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bouquelerec, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247.155A  
; EARLIER FILING DATE: 1999-02-09  
; EARLIER FILING DATE: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER FILING DATE: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER FILING DATE: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER FILING DATE: 60/099,273  
; EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 149  
; LENGTH: 940  
; TYPE: DNA  
; ORGANISM: Homo sapiens

## ; FEATURE:

; NAME/KEY: CDS  
; LOCATION: 177..569  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 177..236  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 11.1999998092651  
; OTHER INFORMATION: seq AFLLLVALSYTLA/RD  
; FEATURE:  
; NAME/KEY: polyA\_site  
; LOCATION: 931..939  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 482  
; OTHER INFORMATION: n=a, g, c o r t  
; OTHER INFORMATION: n=a, g, c o r t

## US-09-247-155-149

Alignment Scores:  
Pred. No.: 5.15e-107 Length: 940  
Score: 914.00 Matches: 188  
Percent Similarity: 90.82% Conservative: 0  
Best Local Similarity: 90.82% Mismatches: 12  
Query Match: 85.98% Indels: 8  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-247-155-149 (1-940)

Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
Db 103 AGACTCAGCTGTGTGTCGACACTCAGAAGCTT-GGACCGCATCTCGCCGCGACTCACA 161

Qy 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
Db 162 CAAGGC-----AGAGTTGCCATGGAAAAAATTCAGTGTTCAGCATTC 203  
Qy 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
Db 204 TTCTCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACACACAGTCAACCTGGAGCC 263  
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
Db 264 AAAAGACACAAAGGACTCTCGACCAAACTGCCAGACCTCTCCAGAGTTGGGGT 323  
Qy 81 AspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
Db 324 GACCAACTCATCTGGACACACACATATGAARAARCTCTATWTAAATCCAAACAAGCAAC 383  
Qy 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
Db 384 AAACCTTGTATGATATTATTCATCACTTGGATGADTGGCCACACAGTCAAGCTTTAAAAAAA 443  
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
Db 444 KTGTTTGTCTGAAATAAARAAATCCAGAAATGGCARANCAGTTTGTCTCCCAATCTG 503  
Qy 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrVal-ProArgIleMe 160  
Db 504 GTTTATGAAACAACTGACAAACACCTTCTCTGTATGGCCAAATATKTCCTCCCGGATAT 563  
Qy 160 tPheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLe 180  
Db 564 GTTTGTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAGATATTTCAAAYCGTCT 623  
Qy 180 uTyrAlaTyrGluProAlaAspThrAlaLeuLeuAspAsnMetLysLysAlaLeuLy 200  
Db 624 CTATGCTTACGAACCTGCGAGATACAGTCTGTGTGTTGACACATGAAGAAGAAAGCTCAA 683  
Qy 200 sLeuLeuLysThrGluLeu 206  
Db 684 GTTGCTGAAGACTGAATTG 702

## RESULT 4

US-09-040-984-78  
; Sequence 78, Application US/09040984  
; Patent No. 6210883  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Wang, Tongtong  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS  
; TITLE OF INVENTION: OF LUNG CANCER  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/040,984  
; FILING DATE: 18-MAR-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.456  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900

```
; TELEFAX: 206-282-6031
; TELEX:
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-040-984-78

Alignment Scores:
Pred. No.: 8.57e-100 Length: 793
Score: 856.50 Matches: 177
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 93.16% Mismatches: 9
Query Match: 80.57% Indels: 3
DB: Gaps: 1

US-09-674-266A-181 (1-206) x US-09-040-984-78 (1-793)

QY 14 HisProSerArgGlyLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGlu 33
Db 2 CATCTAGCGCGCGACTCACAAAGGCGAGTGGTGAGGAAATCCAGAGTTGCCATGGAG 61
QY 34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53
Db 62 AAAATTCAGTGTACAGATTCCTGCTTGTGGCCCTCTCTACACTCTGCCAGAGAT 121
QY 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
Db 122 ACCACAGTCAAACTGGAGCGCAAAAGGACACAAAGGACTCTCGACCCAACTGCCCCAG 181
QY 74 ThrLeuSerArgGlyTrpGlyAspGlnLeuIleThrGlnThrTyrGluGluAlaLeu 93
Db 182 ACCCTCTCAGAGTTGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTTA 241
QY 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCysPro 113
Db 242 TATAATCCAGACAGCAACAAACCTTGATGATTATTCATCATCTGGATGATGCCCA 301
QY 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133
Db 302 CACAGTCNAGCTTTAAAGAAAGTGTGTCTGAAAAATAAGAAATCCAGAAATGGCAGAG 361
QY 134 GlnPheValLeuLeuAsnLysValTyrGluThrThrAspLysHisLeuSerProAspGly 153
Db 362 CAGTTTGTCTCTCAATCTGGTTATGAACAACTGACAAACACCTTTCTCTGATGC 421
QY 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
Db 422 CAGTATGT-CCAGGATTAATGTTTGTGACCCCATCTCTACAGTTGAGCCGATATCCTG 480
QY 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAsp 193
Db 481 GGAAGATATTCAACCGCTCTATGCTTACAAACT-GCAGATACGCTCTGTTGCTTGACA 539
QY 194 AsnMetLysLysAlaLeuLysLeuLys 203
Db 540 CAT---GAAAAGCTCTCAAGTTGCTNAA 566

RESULT 5
US-09-123-912-78
; Sequence 78, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: 09/040,802
; PRIOR FILING DATE: 1998-03-18
```

```
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 793
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (309)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (492)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (563)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (657)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (660)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (703)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (708)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (710)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (711)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (732)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (740)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (748)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (758)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (762)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (765)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (787)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-78

Alignment Scores:
Pred. No.: 8.57e-100 Length: 793
Score: 856.50 Matches: 177
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 93.16% Mismatches: 9
Query Match: 80.57% Indels: 3
DB: Gaps: 1

US-09-674-266A-181 (1-206) x US-09-123-912-78 (1-793)

QY 14 HisProSerArgGlyLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGlu 33
Db 2 CATCTAGCGCGCGACTCACAAAGGCGAGTGGTGAGGAAATCCAGAGTTGCCATGGAG 61
QY 34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53
```

Db 62 AAAATTCAGTGTGAGCAATCTTCTGCTCTGCGCCCTCTCTACACTCTGCGCCAGAGAT 121  
Qy 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73  
Db 122 ACCACAGTCAAACTGGAGCCAAAGGACACAAAGGACTCTCGACCAAACTGCCCCAG 181  
Qy 74 ThrLeuSerArgGlyTyrGlyAspGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 93  
Db 182 ACCCTCTCCAGAGGTGGGGTGAGCAACTCTCTGAGCTCAGACATATGAGAAAGCTCTA 241  
Qy 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCysPro 113  
Db 242 TATTAATCCAGACAGCAAACTCTGAGTATTAATCACTTGGAGTGGAGTGGCCCA 301  
Qy 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133  
Db 302 CACAGTCNAGCTTTAAAGAAAGTGTTCCTGAAATAAAGAAATCCAGAAATGGCAGAG 361  
Qy 134 GlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAspGly 153  
Db 362 CAGTTTGTCTCTCAATCTGGTTTATGAACAACCTGACAAACCTCTCTCTCTGATGGC 421  
Qy 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValAlaGluAspIleThr 173  
Db 422 CAGTATGT-CCAGGATTTATGTTGACCCCTCTCTGACAGTTGAGCGGATATCTCTG 480  
Qy 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAsp 193  
Db 481 GGAAGATATTCAACCGTCTCTATGCTTACAACT-CCAGATACGCTCTGTGCTTGACA 539  
Qy 194 AsnMetLysLysAlaLeuLysLeuLeuLys 203  
Db 540 CAT---GAAAAAGCTCTCAAGTTGCTNAAA 566

## RESULT 6

US-09-643-597-78

; Sequence 78, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 78

; LENGTH: 793

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(793)

; OTHER INFORMATION: n = A, T, C or G

US-09-643-597-78

Alignment Scores:

Pred. No.: 8.57e-100 Length: 793

Score: 856.50 Matches: 177

Percent Similarity: 94.74% Conservative: 3

Best Local Similarity: 93.16% Mismatches: 9

Query Match: 80.57% Indels: 3

Db: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-643-597-78 (1-793)

Qy 14 HisProSerArgArgLeuThrGlnGlyArgTyrValArgLysSerArgValAlaMetGlu 33  
Db 2 CATCTTAGCCGCGACTCACAAAGGAGGTGGGTGAGGAAATCCAGAGTTGCCATGGAG 61  
Qy 34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaAsp 53  
Db 62 AAAATTCAGTGTGAGCAATCTTCTGCTCTGCGCCCTCTCTACACTCTGCGCCAGAT 121  
Qy 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73  
Db 122 ACCACAGTCAAACTGGAGCCAAAGGACACAAAGGACTCTCGACCAAACTGCCCCAG 181  
Qy 74 ThrLeuSerArgGlyTyrGlyAspGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 93  
Db 182 ACCCTCTCCAGAGGTGGGGTGAGCAACTCTCTGAGCTCAGACATATGAGAAAGCTCTA 241  
Qy 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCysPro 113  
Db 242 TATTAATCCAGACAGCAAACTCTGAGTATTAATCACTTGGAGTGGAGTGGCCCA 301  
Qy 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133  
Db 302 CACAGTCNAGCTTTAAAGAAAGTGTTCCTGAAATAAAGAAATCCAGAAATGGCAGAG 361  
Qy 134 GlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAspGly 153  
Db 362 CAGTTTGTCTCTCAATCTGGTTTATGAACAACCTGACAAACCTCTCTCTCTGATGGC 421  
Qy 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValAlaGluAspIleThr 173  
Db 422 CAGTATGT-CCAGGATTTATGTTGACCCCTCTCTGACAGTTGAGCGGATATCTCTG 480  
Qy 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAsp 193  
Db 481 GGAAGATATTCAACCGTCTCTATGCTTACAACT-CCAGATACGCTCTGTGCTTGACA 539  
Qy 194 AsnMetLysLysAlaLeuLysLeuLeuLys 203  
Db 540 CAT---GAAAAAGCTCTCAAGTTGCTNAAA 566

## RESULT 7

US-09-480-884A-78

; Sequence 78, Application US/09480884A

; Patent No. 6482597

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C6

; CURRENT APPLICATION NUMBER: US/09/480,884A

; CURRENT FILING DATE: 2001-08-27

; NUMBER OF SEQ ID NOS: 330

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 78

; LENGTH: 793

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(793)

; OTHER INFORMATION: n = A, T, C or G

US-09-480-884A-78

Alignment Scores:

Pred. No.: 8.57e-100 Length: 793

```
Score: 856.50 Matches: 177
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 93.16% Mismatches: 9
Query Match: 80.57% Indels: 3
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-480-884A-78 (1-793)

QY 14 HisProSerArgLeuThrGlnGlyArgTTPValArgLysSerArgValAlaMetGlu 33
DB 2 CATCTAGCGCCGACTCACACAGGCGAGTGGTGGAGAAATCCAGAGTTGCCATGGAG 61
QY 34 LysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53
DB 62 AAAATTCAGTGTTCAGCATTTCTGCTTGTGGCCCTCTCTACACTCTGGCCAGAT 121
QY 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
DB 122 ACCACAGTCAAACTCGAGCCAAAAGGACACAAAGGACTCTCGACCCAACTGCCCCAG 181
QY 74 ThrLeuSerArgGlyTTPGlyAspGlnLeuileTTPThrGlnThrTyrGluGluAlaLeu 93
DB 182 ACCCTCTCCAGAGGTGGGGTGACCACTCATCTGGACTCAGACATATGAAGAAGCTCTA 241
QY 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysPro 113
DB 242 TATAAATCCAGACAGCAACAAACCTTGATGATTATTCATCTTGGATGAGTCCCA 301
QY 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluileGlnLysLeuAlaGlu 133
DB 302 CACAGTCNAGCTTTAAAGAAAGTGTGCTGAAAAATAAGAAATCCAGAAATGGCAGAG 361
QY 134 GlnPheValLeuLeuAsnLysValPheAlaGluAsnLysGluileGlnLysLeuAlaGlu 153
DB 362 CAGTTTGTCTCTCAATCTGTTTATGAACAACTGACAAACACCTTTCTCTGATGGC 421
QY 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
DB 422 CAGTAGT-CCAGGATTATGTTTGTGACCCATCTCTGACAGTTGAAGCCGATATCTTG 480
QY 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuAsp 193
DB 481 GGAAGATATTCAACCGTCTCTATGCTTACAAACT-GCAGATACGCTCTGTTGCTTGACA 539

RESULT 8
US-09-542-615A-78
; Sequence 78, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-04-14
; SOFTWARE: FastSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 78
; LENGTH: 793
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(793)

; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-78
Alignment Scores:
Pred. No.: 8.57e-100 Length: 793
Score: 856.50 Matches: 177
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 93.16% Mismatches: 9
Query Match: 80.57% Indels: 3
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-542-615A-78 (1-793)

QY 14 HisProSerArgLeuThrGlnGlyArgTTPValArgLysSerArgValAlaMetGlu 33
DB 2 CATCTAGCGCCGACTCACACAGGCGAGTGGTGGAGAAATCCAGAGTTGCCATGGAG 61
QY 34 LysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53
DB 62 AAAATTCAGTGTTCAGCATTTCTGCTTGTGGCCCTCTCTACACTCTGGCCAGAT 121
QY 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
DB 122 ACCACAGTCAAACTCGAGCCAAAAGGACACAAAGGACTCTCGACCCAACTGCCCCAG 181
QY 74 ThrLeuSerArgGlyTTPGlyAspGlnLeuileTTPThrGlnThrTyrGluGluAlaLeu 93
DB 182 ACCCTCTCCAGAGGTGGGGTGACCACTCATCTGGACTCAGACATATGAAGAAGCTCTA 241
QY 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysPro 113
DB 242 TATAAATCCAGACAGCAACAAACCTTGATGATTATTCATCTTGGATGAGTCCCA 301
QY 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluileGlnLysLeuAlaGlu 133
DB 302 CACAGTCNAGCTTTAAAGAAAGTGTGCTGAAAAATAAGAAATCCAGAAATGGCAGAG 361
QY 134 GlnPheValLeuLeuAsnLysValPheAlaGluAsnLysGluileGlnLysLeuAlaGlu 153
DB 362 CAGTTTGTCTCTCAATCTGTTTATGAACAACTGACAAACACCTTTCTCTGATGGC 421
QY 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
DB 422 CAGTAGT-CCAGGATTATGTTTGTGACCCATCTCTGACAGTTGAAGCCGATATCTTG 480
QY 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuAsp 193
DB 481 GGAAGATATTCAACCGTCTCTATGCTTACAAACT-GCAGATACGCTCTGTTGCTTGACA 539

RESULT 9
US-09-606-421B-78
; Sequence 78, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
```

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 78  
LENGTH: 793  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(793)  
OTHER INFORMATION: n = A,T,C or G  
US-09-606-421B-78

Alignment Scores:  
Pred. No.: 8.57e-100 Length: 793  
Score: 856.50 Matches: 177  
Percent Similarity: 94.74% Conservative: 3  
Best Local Similarity: 93.16% Mismatches: 9  
Query Match: 80.57% Indels: 3  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-606-421B-78 (1-793)

QY 14 HisProSerArgArgLeuThrGlnGlyArgTIPValAlaMetGlu 33  
DB 2 CATCTAGCCCGGACTCACACAGGCGAGTGGGTGAGGAATCCAGATGGCATGGAG 61  
QY 34 LysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53  
DB 62 AAAATCCAGTGTCCAGCATCTTCTCTGTGGCCCTCTCTACACTCTGGCCAGAT 121  
QY 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73  
DB 122 ACCACAGTCAAACTCGAGGCGAAAGACACAAAGGAGCTCTGACCAAACTGCCCCAG 181  
QY 74 ThrLeuSerArgGlyTTPGlyAspGlnLeuLeuThrGlnThrTyrGluGluAlaLeu 93  
DB 182 ACCTCTCCAGAGTGGGTGGGACCACTCATCTGGACTCAGACATAGGAAGCTCTA 241  
QY 94 TyLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCysPro 113  
DB 242 TATAAATCCAGACACAAACCTCTGATGATTATTCATCATCTGGATGAGTGCCCA 301  
QY 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGlu 133  
DB 302 CACAGTCNAGCTTTAAAGAAAGTGTGTCTGAAATAAAGAAATCCAGAAATGGCAG 361  
QY 134 GlnPheValLeuLeuLeuValTyrGluThrThrAspLysHisLeuSerProAspGly 153  
DB 362 CAGTTTCTCTCTCAATCTGGTTATGAAACCACTGACAAACACCTTTCTCTGATGGC 421  
QY 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleThr 173  
DB 422 CAGTATGT-CCAGGATTATGTTGTGACCCATCTCTGACAGTTGAAGCCGATATCCTG 480  
QY 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuAsp 193  
DB 481 GGAAGATATTCAAAACCTCTCTATGCTTACAACT-CCAGATACGCTCTGTGTGTTGACA 539  
QY 194 AsnMetLysLysAlaLeuLysLeuLys 203  
DB 540 CAT---GAAAAAGCTCTCAAGTTGCTNAAA 566

RESULT 10

US-09-221-298-32  
Sequence 32, Application US/09221298  
Patent No. 6284241  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS  
FILE REFERENCE: 210121.471  
CURRENT APPLICATION NUMBER: US/09/221,298  
CURRENT FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 401  
TYPE: DNA  
ORGANISM: Human  
US-09-221-298-32

Alignment Scores:  
Pred. No.: 4.05e-78 Length: 401  
Score: 683.00 Matches: 132  
Percent Similarity: 98.51% Conservative: 0  
Best Local Similarity: 98.51% Mismatches: 1  
Query Match: 64.25% Indels: 1  
DB: 3 Gaps: 0

US-09-674-266A-181 (1-206) x US-09-221-298-32 (1-401)

QY 57 LysProGlyAlaLysLysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSer 76  
DB 2 AAACCTGGAGCCCAAAAGGACACAAAGGAGCTCTGACCAAACTGCCCCAGACCTCTCC 61  
QY 77 ArgGlyTTPGlyAspGlnLeuIleTTPThrGlnThrTyrGluGluAlaLeuTyrLysSer 96  
DB 62 AGAGGTGGGGTGACCAACTCATCTGACTCAGACATATGAAGAAGCTCTATATAAATCC 121  
QY 97 LysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCysProHisSerGln 116  
DB 122 AAGACAGACACAAACCTTGATGATTATTCATCTGGGTGAGTGCCACACAGTCAA 181  
QY 117 AlaLeuLysLysValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGluInPheVal 136  
DB 182 GCTTTAAAGAAAGTGTGTCTGAAATAAAGAAATCCAGAAATGGCAGAGCAGTTTGTTC 241  
QY 137 LeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrVal 156  
DB 242 CTCTCAATCTGGTTATGAAACCACTGACAAACACCTTTCTCTGATGCCAGTATGTC 301  
QY 157 ProArgIleMetPheValAspProSerLeuThrValArgAla-AspIleThrGlyArgTyr 176  
DB 302 CCAGGATTATGTTGTGACCCATCTCTGACAGTTAGAGCCCGATATCACTGGAAGNTA 361

RESULT 11

US-08-916-576B-35  
Sequence 35, Application US/08916576B  
Patent No. 6171816  
GENERAL INFORMATION:  
APPLICANT: YU, GUO-LIANG  
APPLICANT: DILLON, PATRICK J.  
APPLICANT: EBNER, REINHARD  
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/916,576B  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:





TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(404)  
OTHER INFORMATION: n = A,T,C or G  
US-09-480-884A-282

Alignment Scores:  
Pred. No.: 1.77e-71 Length: 404  
Score: 631.00 Matches: 125  
Percent Similarity: 92.59% Conservative: 0  
Best Local Similarity: 92.59% Mismatches: 4  
Query Match: 59.36% Indels: 6  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-480-884A-282 (1-404)

```
Qy 13 ProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMet 32
Db 16 CCGCATCTTANNCGCGGACTCACAAAGGC-----AGAGTNGCCCATG 57
Qy 33 GlulysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArg 52
Db 58 GAGAAAATTCAGTGTCCAGTCTTCTCTCTTGTGGCCCTCTCTACACTCTGGCCAGA 117
Qy 53 AspThrThrValLysProGlyAlaLysAspThrLysAspSerArgProLysLeuPro 72
Db 118 GATACCACTCAACCTGNAGCCAAAGGACACAAAGGACTCTGACCCAAACTGCC 177
Qy 73 GlnThrLeuSerArgGlyTrpGlyAspGlnLeuLeuTrpThrGlnThrTyrGluGluAla 92
Db 178 CANACCCTCTCCAGAGGTGGGGTGACCAACTCATCTGGACTCANACATATGAAGAAGCT 237
Qy 93 LeuTyrLysSerLysThrSerAsnLysProLeuMetIleHleHisLeuAspGluCys 112
Db 238 CTATATAAATCCAGACAGCAACAAACCCTTGATGATTATTCATCACTTTGGATGAGTGC 297
Qy 113 ProHisSerGlnAlaLeuLysValPheAlaGluAsnLysGluIleGlnLysLeuAla 132
Db 298 CCACACAGTCNAGCTTTAAGAAAGTGTTCCTGAAATAAAGAAATCCAGAAATTTGGCA 357
Qy 133 GluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLys 147
Db 358 GAGCAGTTTGTCTCTCAATCTGGTTTATGAAACAACTGACAAA 402
```

## RESULT 14

US-09-542-615A-282  
Sequence 282, Application US/09542615A  
Patent No. 6518256  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542.615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 282  
LENGTH: 404  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(404)  
OTHER INFORMATION: n = A,T,C or G  
US-09-542-615A-282

## Alignment Scores:

Pred. No.: 1.77e-71 Length: 404  
Score: 631.00 Matches: 125  
Percent Similarity: 92.59% Conservative: 0  
Best Local Similarity: 92.59% Mismatches: 4  
Query Match: 59.36% Indels: 6  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-542-615A-282 (1-404)

```
Qy 13 ProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMet 32
Db 16 CCGCATCTTANNCGCGGACTCACAAAGGC-----AGAGTNGCCCATG 57
Qy 33 GlulysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArg 52
Db 58 GAGAAAATTCAGTGTCCAGTCTTCTCTCTTGTGGCCCTCTCTACACTCTGGCCAGA 117
Qy 53 AspThrThrValLysProGlyAlaLysAspThrLysAspSerArgProLysLeuPro 72
Db 118 GATACCACTCAACCTGNAGCCAAAGGACACAAAGGACTCTGACCCAAACTGCC 177
Qy 73 GlnThrLeuSerArgGlyTrpGlyAspGlnLeuLeuTrpThrGlnThrTyrGluGluAla 92
Db 178 CANACCCTCTCCAGAGGTGGGGTGACCAACTCATCTGGACTCANACATATGAAGAAGCT 237
Qy 93 LeuTyrLysSerLysThrSerAsnLysProLeuMetIleHleHisLeuAspGluCys 112
Db 238 CTATATAAATCCAGACAGCAACAAACCCTTGATGATTATTCATCACTTTGGATGAGTGC 297
Qy 113 ProHisSerGlnAlaLeuLysValPheAlaGluAsnLysGluIleGlnLysLeuAla 132
Db 298 CCACACAGTCNAGCTTTAAGAAAGTGTTCCTGAAATAAAGAAATCCAGAAATTTGGCA 357
Qy 133 GluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLys 147
Db 358 GAGCAGTTTGTCTCTCAATCTGGTTTATGAAACAACTGACAAA 402
```

## RESULT 15

US-09-606-421B-282  
Sequence 282, Application US/09606421B  
Patent No. 6531315  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606.421B  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 282  
LENGTH: 404  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(404)  
OTHER INFORMATION: n = A,T,C or G  
US-09-606-421B-282

## Alignment Scores:

Pred. No.: 1.77e-71 Length: 404  
Score: 631.00 Matches: 125

Percent Similarity: 92.59%  
 Best Local Similarity: 92.59%  
 Query Match: 59.36%  
 DB: 4  
 Conservative: 0  
 Mismatches: 4  
 Indels: 6  
 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-606-421B-282 (1-404)

QY	13	ProHisProSerArgLeuThrGlnGlyArgTyrValArgLysSerArgValAlaMet	32
DB	16	CGCATCTCTANNCGCGACTCACACAGGC-----AGAGTNGCCATG	57
QY	33	GluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLeuAlaArg	52
DB	58	GAGAAAATCCAGTGTCCAGATTCTTGTCTCTTGTGGCCCTCTCTACACTCTGGCCAGA	117
QY	53	AspThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuPro	72
DB	118	GATACCACAGTCAAACTGNAGCCAAAAGGACACAAAGGACTCTCGACCCAAACTGCC	177
QY	73	GlnThrLeuSerArgGlyTyrGlyAspGlnLeuIleTyrThrGlnThrTyrGluAla	92
DB	178	CANACCTCTCCAGAGTTGGGGTGACCAACTCATCTGGACTCANACATATGAGAAGCT	237
QY	93	LeuTyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCys	112
DB	238	CTATATAAATCCAAGACACAGCAACAAACCCCTTCATGATTATTTCATCATCTGGATGAGTGC	297
QY	113	ProHisSerGlnAlaLeuLysValPheAlaGluAsnLysGluIleGlnLysLeuAla	132
DB	298	CCACACAGTCAAGCTTTAAAGAAAGTGTGTGCTGAAAAATAAAGAAATCCAGAAATTTGGCA	357
QY	133	GluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLys	147
DB	358	GAGCAGTTTGTCTCTCTCAATCTGGTTATGAAACAACTGACANA	402

Search completed: November 30, 2003, 04:51:26  
 Job time : 67 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2003, 15:55:59 ; Search time 31 Seconds  
(without alignments)  
1225.655 Million cell updates/sec

Title: US-09-674-266a-181

Perfect score: 1063

Sequence: 1 RLSCAGTSLSGPHSRRLT.....DTALLDNMKKALKLKTTEL 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1002	94.3	202	15	US-10-106-698-6395
2	899	84.6	175	10	US-09-792-439-2
3	899	84.6	175	12	US-10-237-496-28
4	899	84.6	175	12	US-10-242-074-28
5	899	84.6	175	12	US-10-242-505-28
6	899	84.6	175	12	US-10-242-574-28
7	899	84.6	175	12	US-10-243-261-28
8	899	84.6	175	12	US-10-243-282-28
9	899	84.6	175	12	US-10-243-402-28
10	899	84.6	175	12	US-10-243-431-28
11	899	84.6	175	12	US-10-245-164-28
12	899	84.6	175	12	US-09-903-190-106
13	899	84.6	175	12	US-10-244-972-28
14	899	84.6	175	12	US-10-197-942-28
15	899	84.6	175	12	US-10-238-196-28

16	899	84.6	175	12	US-10-245-013-28	Sequence 28, Appl
17	899	84.6	175	15	US-10-078-337-2	Sequence 2, Appl
18	899	84.6	175	15	US-10-245-103-28	Sequence 28, Appl
19	899	84.6	175	15	US-10-245-107-28	Sequence 28, Appl
20	899	84.6	175	15	US-10-245-143-28	Sequence 28, Appl
21	899	84.6	175	15	US-10-245-771-28	Sequence 28, Appl
22	899	84.6	175	15	US-10-245-851-28	Sequence 28, Appl
23	899	84.6	175	15	US-10-245-883-28	Sequence 28, Appl
24	899	84.6	175	15	US-10-237-535-28	Sequence 28, Appl
25	899	84.6	175	15	US-10-238-183-28	Sequence 28, Appl
26	899	84.6	175	15	US-10-238-283-28	Sequence 28, Appl
27	899	84.6	175	15	US-10-238-370-28	Sequence 28, Appl
28	899	84.6	175	15	US-10-245-055-28	Sequence 28, Appl
29	899	84.6	175	15	US-10-245-147-28	Sequence 28, Appl
30	899	84.6	175	15	US-10-245-730-28	Sequence 28, Appl
31	899	84.6	175	15	US-10-245-739-28	Sequence 28, Appl
32	899	84.6	175	15	US-10-246-210-28	Sequence 28, Appl
33	899	84.6	175	15	US-10-239-196-28	Sequence 28, Appl
34	899	84.6	175	15	US-10-243-024-28	Sequence 28, Appl
35	899	84.6	175	15	US-10-243-409-28	Sequence 28, Appl
36	899	84.6	175	15	US-10-245-621-28	Sequence 28, Appl
37	899	84.6	175	15	US-10-245-880-28	Sequence 28, Appl
38	899	84.6	175	15	US-10-245-033-28	Sequence 28, Appl
39	899	84.6	175	15	US-10-243-095-28	Sequence 28, Appl
40	899	84.6	175	15	US-10-245-185-28	Sequence 28, Appl
41	899	84.6	175	15	US-10-245-427-28	Sequence 28, Appl
42	899	84.6	175	15	US-10-245-473-28	Sequence 28, Appl
43	899	84.6	175	15	US-10-245-770-28	Sequence 28, Appl
44	899	84.6	175	15	US-10-245-877-28	Sequence 28, Appl
45	899	84.6	175	15	US-10-246-976-28	Sequence 28, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-106-698-6395

; Sequence 6395, Application US/10106698

; Publication No. US20030109690A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

; FILE REFERENCE: PA00SP1

; CURRENT APPLICATION NUMBER: US/10106.698

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: PCT/US00/26524

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/157,137

; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: US 60/163,280

; NUMBER OF SEQ ID NOS: 8564

; SOFTWARE: Patentin ver. 3.0

; SEQ ID NO 6395

; LENGTH: 202

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: MISC FEATURE

; LOCATION: (7)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-106-698-6395

Query Match

Best Local Similarity 94.3%; Score 1002; DB 15; Length 202;

Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PHSRRLLTQGRVWRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKTDKSRKLP 72

Db 9 PHSRRLLTQGRVWRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKTDKSRKLP 68

QY 73 QTLRSGDQLIWTTQYEEALYKSTSNKPLMIHLLDECPHSQALKKVFPAENKEIQKLA 132  
DB 69 QTLRSGDQLIWTTQYEEALYKSTSNKPLMIHLLDECPHSQALKKVFPAENKEIQKLA 128  
QY 133 EQVLLNLVYETTDKHLSPDQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLL 192  
DB 129 EQVLLNLVYETTDKHLSPDQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLL 188  
QY 193 DNMKKALKLLKTEL 206  
DB 189 DNMKKALKLLKTEL 202

## RESULT 2

US-09-792-439-2  
; Sequence 2, Application US/09792439  
; Patent No. US20020111303A1  
; GENERAL INFORMATION:  
; APPLICANT: Boyd, Robert Simon  
; APPLICANT: Stamps, Alasdair Craig  
; APPLICANT: Terratt, Jonathan Alexander  
; APPLICANT: Tyson, Kerry Louise  
; TITLE OF INVENTION: Diagnostic and Therapeutic Methods  
; FILE REFERENCE: 2543-1-005N  
; CURRENT APPLICATION NUMBER: US/09/792,439  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: GB 0004576.5  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: human  
US-09-792-439-2

Query Match 84.6%; Score 899; DB 10; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 MEKIPVSFLLLVALLSYTLARDTTVKPGAKKDTKDSRPKLPQTLRSGDQLIWTTQYEE 91  
DB 1 MEKIPVSFLLLVALLSYTLARDTTVKPGAKKDTKDSRPKLPQTLRSGDQLIWTTQYEE 60  
QY 92 ALYKSTSNKPLMIHLLDECPHSQALKKVFPAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
DB 61 ALYKSTSNKPLMIHLLDECPHSQALKKVFPAENKEIQKLAQFVLLNLVYETTDKHLSP 120  
QY 152 DQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206  
DB 121 DQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 175

## RESULT 3

US-10-237-496-28  
; Sequence 28, Application US/10237496  
; Publication No. US20030138896A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3630R1C4  
; CURRENT APPLICATION NUMBER: US/10/237,496  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-237-496-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 MEKIPVSFLLLVALLSYTLARDTTVKPGAKKDTKDSRPKLPQTLRSGDQLIWTTQYEE 91  
DB 1 MEKIPVSFLLLVALLSYTLARDTTVKPGAKKDTKDSRPKLPQTLRSGDQLIWTTQYEE 60  
QY 92 ALYKSTSNKPLMIHLLDECPHSQALKKVFPAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
DB 61 ALYKSTSNKPLMIHLLDECPHSQALKKVFPAENKEIQKLAQFVLLNLVYETTDKHLSP 120  
QY 152 DQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206  
DB 121 DQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 175

## RESULT 4

US-10-242-074-28  
; Sequence 28, Application US/10242074  
; Publication No. US20030138897A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C19  
; CURRENT APPLICATION NUMBER: US/10/242,074  
; CURRENT FILING DATE: 2002-09-11  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 30, 2003, 03:27:12 ; Search time 308 Seconds

(without alignments)  
2203.591 Million cell updates/sec

Title: US-09-674-266A-181

Perfect score: 1063

Sequence: 1 RLSCAGTSGSGPHPSRLT.....DTALLDNMKALKLKTLEL 206

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh  
-MODEL=frame+ p2n.model  
-Q=/cgn2\_1/USPTO spo01/US09674266/runat\_26112003\_152750\_15846/app\_query.fasta\_1.391  
-DB=PublishedApplications NA -QWMS=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPECL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USERS=US09674266 @CNC 1.1 221 @runat\_26112003\_152750\_15846  
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1025	96.4	920	12	US-10-237-496-27

Sequence 27, Appl

2	1025	96.4	920	12	US-10-242-074-27	Sequence 27, Appl
3	1025	96.4	920	12	US-10-242-505-27	Sequence 27, Appl
4	1025	96.4	920	12	US-10-242-574-27	Sequence 27, Appl
5	1025	96.4	920	12	US-10-243-261-27	Sequence 27, Appl
6	1025	96.4	920	12	US-10-243-282-27	Sequence 27, Appl
7	1025	96.4	920	12	US-10-243-402-27	Sequence 27, Appl
8	1025	96.4	920	12	US-10-243-431-27	Sequence 27, Appl
9	1025	96.4	920	12	US-10-245-164-27	Sequence 27, Appl
10	1025	96.4	920	12	US-10-244-972-27	Sequence 27, Appl
11	1025	96.4	920	12	US-10-197-942-27	Sequence 27, Appl
12	1025	96.4	920	12	US-10-238-196-27	Sequence 27, Appl
13	1025	96.4	920	12	US-10-245-013-27	Sequence 27, Appl
14	1025	96.4	920	14	US-10-245-103-27	Sequence 27, Appl
15	1025	96.4	920	14	US-10-245-107-27	Sequence 27, Appl
16	1025	96.4	920	14	US-10-245-143-27	Sequence 27, Appl
17	1025	96.4	920	14	US-10-245-771-27	Sequence 27, Appl
18	1025	96.4	920	14	US-10-245-851-27	Sequence 27, Appl
19	1025	96.4	920	14	US-10-245-883-27	Sequence 27, Appl
20	1025	96.4	920	14	US-10-237-535-27	Sequence 27, Appl
21	1025	96.4	920	14	US-10-238-183-27	Sequence 27, Appl
22	1025	96.4	920	14	US-10-238-283-27	Sequence 27, Appl
23	1025	96.4	920	14	US-10-238-370-27	Sequence 27, Appl
24	1025	96.4	920	14	US-10-245-055-27	Sequence 27, Appl
25	1025	96.4	920	14	US-10-245-147-27	Sequence 27, Appl
26	1025	96.4	920	14	US-10-245-730-27	Sequence 27, Appl
27	1025	96.4	920	14	US-10-245-739-27	Sequence 27, Appl
28	1025	96.4	920	14	US-10-246-210-27	Sequence 27, Appl
29	1025	96.4	920	14	US-10-239-196-27	Sequence 27, Appl
30	1025	96.4	920	14	US-10-243-024-27	Sequence 27, Appl
31	1025	96.4	920	14	US-10-243-409-27	Sequence 27, Appl
32	1025	96.4	920	14	US-10-245-621-27	Sequence 27, Appl
33	1025	96.4	920	14	US-10-245-880-27	Sequence 27, Appl
34	1025	96.4	920	14	US-10-245-033-27	Sequence 27, Appl
35	1025	96.4	920	14	US-10-243-095-27	Sequence 27, Appl
36	1025	96.4	920	14	US-10-245-185-27	Sequence 27, Appl
37	1025	96.4	920	14	US-10-245-427-27	Sequence 27, Appl
38	1025	96.4	920	14	US-10-245-473-27	Sequence 27, Appl
39	1025	96.4	920	14	US-10-245-770-27	Sequence 27, Appl
40	1025	96.4	920	14	US-10-245-877-27	Sequence 27, Appl
41	1025	96.4	920	14	US-10-246-976-27	Sequence 27, Appl
42	1025	96.4	920	14	US-10-243-320-27	Sequence 27, Appl
43	1025	96.4	920	14	US-10-242-743-27	Sequence 27, Appl
44	1025	96.4	920	14	US-10-242-845-27	Sequence 27, Appl
45	1025	96.4	920	14	US-10-237-636-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1  
US-10-237-496-27  
; Sequence 27, Application US/10237496  
; Publication No. US20030138896A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C4  
; CURRENT APPLICATION NUMBER: US/10/237,496  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 27  
LENGTH: 920  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-237-496-27

Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservatives: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: Gaps: 0

US-09-674-266A-181 (1-206) x US-10-237-496-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
DB 56 AGACTCAGCTGTGTCGACACACACAGAGCTT-GGACCGCATCTAGCCGCCGACTCACA 114  
QY 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGlnLysLysProValSerAlaPhe 40  
DB 115 CAAGGCGAGTGGGTGAGGAAATCCAGAGTTGCCATGGAGAAATTCAGTGTCCAGCATTC 174  
QY 41 LeuLeuLeuValAlaLeuSerTyThrLeuAlaArgAspThrThrValLysProGlyAla 60  
DB 175 TTGCTCTTGTGGCCCTCTCTACACTCTGCCAGAGATACACAGTCAAACTTGAGCC 234  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
DB 235 AAAAAAGACAAAGGACTCTGACCCAAACTGCCAGACCTCTCCAGAGTTGGGT 294  
QY 81 AspGlnLeuLeuTrpThrGlnThrTyThrGlnAlaLeuTyLysSerLysThrSerAsn 100  
DB 295 GACCACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAAGCAAGCAAC 354  
QY 101 LysProLeuMetIleLeuHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
DB 355 AAACCTTGTATGATTATTCTATCTATGATGAGTGCACACAGTCAAGCTTTAAGAAA 414  
QY 121 ValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
DB 415 GTGTTTGTCTGAAATAAAGAAATCCAGAAATGGCAGAGCAGTTTGTCTCTCTCAATCTG 474  
QY 141 ValTyThrGlnThrThrAspLysHisLeuSerProAspGlyGlnTyThrValProArgIleMet 160  
DB 475 GTTATGAAACAACTGACAAACACCTTTCTCTGATGGCCAGTATGTCCCGAGATTATG 534  
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyThrSerAsnArgLeu 180  
DB 535 TTTGTTGACCACTCTCTGACAGTTAGAGCCGATATCTCTGGAAGATATTCAATTCGTCTC 594  
QY 181 TyrAlaTyThrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200

DB 595 TATGCTTACGAACCTGCAGATACAGCTCTGTTGTTGACACATGAAGAAAGCTCTCAAG 654  
QY 201 LeuLeuLysThrGluLeu 206  
DB 655 TTGCTGAGAGACTGAATG 672

RESULT 2  
US-10-242-074-27  
Sequence 27, Application US/10242074  
Publication No. US20030138897A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Baton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C19  
CURRENT APPLICATION NUMBER: US/10/242,074  
CURRENT FILING DATE: 2002-09-11  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 27  
LENGTH: 920  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-242-074-27

Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservatives: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: Gaps: 0

US-09-674-266A-181 (1-206) x US-10-242-074-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
DB 56 AGACTCAGCTGTGTCGACACACACAGAGCTT-GGACCGCATCTAGCCGCCGACTCACA 114  
QY 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGlnLysLysProValSerAlaPhe 40  
DB 115 CAAGGCGAGTGGGTGAGGAAATCCAGAGTTGCCATGGAGAAATTCAGTGTCCAGCATTC 174

```
QY 41 LeuLeuLeuValAlaLeuSerThrThrLeuAlaArgAspThrThrValLysProGlyAla 60
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACACAGTCAAACTGGAGCC 234
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLysSerArgGlyTrpGly 80
Db 235 AAAAAGGACACAAAGACTCTCGACCCAACTGCCCCAGACCTCTCCAGAGTTGGGGT 294
QY 81 AspGlnLeuLeuLeuThrThrGlnThrThrGluGluAlaLeuThrLysSerLysThrSerAen 100
Db 295 GACCAACTCATCTGACTCAGACATATGAAGAGCTCTATATAATCCAGACAGCAAC 354
QY 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
Db 355 AAACCTTGTATATTATCATCTGATGGATGAGTCCACACAGTCAAGCTTTAAAGAA 414
QY 121 ValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140
Db 415 GTGTTTGTCTGAAATTAAGAAATCCAGAAATTTGGCAGAGCAGTTTGTCTCTCAATCTG 474
QY 141 ValTyGluThrThrAspLysHisLeuSerProAspGlyGlnThrValProArgIleMet 160
Db 475 GTTATGAACAACCTGACAAACCTTCTCTGATGGCCAGTATGTCCTCCAGGATTATG 534
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTy+SerAsnArgLeu 180
Db 535 TTGTTGACCCATCTCTGACAGTGTAGGCCGATATCACTGGAAGATATTTCAATCTGCTC 594
QY 181 TyrAlaTyGluProAlaAspThrAlaLeuLeuAspAsnMetLysLysAlaLeuLys 200
Db 595 TATGCTTACGAACCTCGCATACAGCTCTGTTGCTTGAACAACATGAAGAAGCTCTCAAG 654
QY 201 LeuLeuLysThrGluLeu 206
Db 655 TTGCTGAAGACTGAATTG 672
```

## RESULT 3

```
US-10-242-505-27
; Sequence 27, Application US/10242505
; Publication No. US2003013898A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C25
; CURRENT APPLICATION NUMBER: US/10/242,505
; CURRENT FILING DATE: 2002-09-11
; PRIORITY APPLICATION NUMBER: 10/197942
; PRIORITY FILING DATE: 2002-07-18
; PRIORITY APPLICATION NUMBER: 60/059114
; PRIORITY FILING DATE: 1997-09-17
; PRIORITY APPLICATION NUMBER: 60/063046
; PRIORITY FILING DATE: 1997-10-24
; PRIORITY APPLICATION NUMBER: 60/065027
; PRIORITY FILING DATE: 1997-11-10
; PRIORITY APPLICATION NUMBER: 60/079689
; PRIORITY FILING DATE: 1998-03-27
; PRIORITY APPLICATION NUMBER: 60/086478
; PRIORITY FILING DATE: 1998-05-22
; PRIORITY APPLICATION NUMBER: 60/087607
; PRIORITY FILING DATE: 1998-06-02
```

```
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 27
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-242-505-27
```

## Alignment Scores:

Pred. No.:	1.33e-130	Length:	920
Score:	1025.00	Matches:	203
Percent Similarity:	98.54%	Conservative:	0
Best Local Similarity:	98.54%	Mismatches:	3
Query Match:	96.43%	Indels:	1
DB:	12	Gaps:	0

US-09-674-266A-181 (1-206) x US-10-242-505-27 (1-920)

```
QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
Db 56 AGACTCAGCTGTGCTGGCAGACTCAGAAAGCTT-GGACCGCATCTTAGCGCGGACTCACA 114
QY 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
Db 115 CAAGCAGGTGGGTGAGGAAATCCAGAGTTGCCATGGAGAAATTTCCAGTGTCCAGATT 174
QY 41 LeuLeuLeuValAlaLeuSerThrThrLeuAlaArgAspThrThrValLysProGlyAla 60
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGCCAGAGATACACAGTCAAACTGGAGCC 234
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80
Db 235 AAAAAGGACACAAAGACTCTCGACCCAACTGCCCCAGACCTCTCCAGAGTTGGGGT 294
QY 81 AspGlnLeuLeuLeuThrThrGlnThrThrGluGluAlaLeuThrLysSerLysThrSerAen 100
Db 295 GACCAACTCATCTGACTCAGACATATGAAGAGCTCTATATAATCCAGACAGCAAC 354
QY 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
Db 355 AAACCTTGTATATTATTCATCACTTGGATGAGTGGCCACACAGTCAAGCTTTAAAGAA 414
QY 121 ValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140
Db 415 GTGTTTGTCTGAAATTAAGAAATCCAGAAATTTGGCAGAGCAGTTTGTCTCTCAATCTG 474
QY 141 ValTyGluThrThrAspLysHisLeuSerProAspGlyGlnThrValProArgIleMet 160
Db 475 GTTATGAACAACCTCGCATACAGCTCTGTTGCTTGAACAACATTTCAATCTGCTC 534
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTy+SerAsnArgLeu 180
Db 535 TTTGTTGACCCATCTCTGACAGTGTAGGCCGATATCACTGGAAGATATTTCAATCTGCTC 594
QY 181 TyrAlaTyGluProAlaAspThrAlaLeuLeuAspAsnMetLysLysAlaLeuLys 200
Db 595 TATGCTTACGAACCTCGCATACAGCTCTGTTGCTTGAACAACATGAAGAAGCTCTCAAG 654
QY 201 LeuLeuLysThrGluLeu 206
Db 655 TTGCTGAAGACTGAATTG 672
```

## RESULT 4

```
US-10-242-574-27
; Sequence 27, Application US/10242574
; Publication No. US2003013899A1
; GENERAL INFORMATION:
```





ORGANISM: Homo Sapien  
US-10-243-261-27

Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-243-261-27 (1-920)

```
QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgLeuThr 20
   |||||
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTTAGCCGCCGACTCACA 114
   |||||
QY 21 GlnGlyArgTTPValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
   |||||
Db 115 CAAGCAGGTGGGTGAGGAATCCAGAGTTGCCATGGAGAAATTCAGTGTTCAGCATTC 174
   |||||
QY 41 LeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
   |||||
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATCCACAGTCAAACTTGAGCC 234
   |||||
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTTPGly 80
   |||||
Db 235 AAAAAGGACACAAAGGACTCTCGACCAAACTGCCAGACCTCTCCAGAGGTTGGGT 294
   |||||
QY 81 AspGlnLeuIleTTPThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
   |||||
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAAGCAAGCAAC 354
   |||||
QY 101 LysProLeuMetIleThiHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
   |||||
Db 355 AAACCTTGATGATTATTCATCTGGATGAGTGGCCACAGTCAGCTTAAAGAAA 414
   |||||
QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuAsnLeu 140
   |||||
Db 415 GTGTTTGTCTGAAATTAAGAAATCCAGAAATTTGGCAGAGCAGCTTTGCTCTCAATCTG 474
   |||||
QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
   |||||
Db 475 GTTTATGAACAACTCACAACACCTTTCTCTGATGGCCAGTATGCTCCAGGATTATG 534
   |||||
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
   |||||
Db 535 TTGTTGACCAATCTCAGACTTGAGCCGATATCAGTGGAGATATTTCAAATCGTCTC 594
   |||||
QY 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
   |||||
Db 595 TATGCTTAGCAACTTCGAGATACAGCTCTGTTGCTTGACACATGAGAAAGCTCTCAAG 654
   |||||
QY 201 LeuLeuLysThrGluLeu 206
   |||||
Db 655 TTGCTGAAGACTGAATTG 672
   |||||
```

## RESULT 6

US-10-243-282-27  
; Sequence 27, Application US/10243282  
; Publication No. US20030138901A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C50  
; CURRENT APPLICATION NUMBER: US/10/243,282  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 27  
; LENGTH: 920  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-243-282-27

Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-243-282-27 (1-920)

```
QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgLeuThr 20
   |||||
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTTAGCCGCCGACTCACA 114
   |||||
QY 21 GlnGlyArgTTPValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
   |||||
Db 115 CAAGCAGGTGGGTGAGGAATCCAGAGTTGCCATGGAGAAATTCAGTGTTCAGCATTC 174
   |||||
QY 41 LeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
   |||||
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGCCAGAGATCCACAGTCAAACTTGAGCC 234
   |||||
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTTPGly 80
   |||||
Db 235 AAAAAGGACACAAAGGACTCTCGACCAAACTGCCAGACCTCTCCAGAGGTTGGGT 294
   |||||
QY 81 AspGlnLeuIleTTPThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
   |||||
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAAGCAAGCAAC 354
   |||||
QY 101 LysProLeuMetIleThiHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
   |||||
Db 355 AAACCTTGATGATTATTCATCTGGATGAGTGGCCACAGTCAGCTTAAAGAAA 414
   |||||
QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuAsnLeu 140
   |||||
Db 415 GTGTTTGTCTGAAATTAAGAAATTCAGAAATTTGGCAGAGCAGCTTTGCTCTCAATCTG 474
   |||||
QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
```

Db 475 GTTATGAAACACTGACAAACACTTCTCTGATGGCCGATATGTCCTCCAGATTATG 534  
Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180  
Db 535 TTTGTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAAATCGTCTC 594  
Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 200  
Db 595 TATGCTTACGAACCTGCGAGATACAGCTCTGTGTTGTTGACCAACATGAAGAAAGCTCTCAAG 654  
Qy 201 LeuLeuLysThrGluLeu 206  
Db 655 TTGCTGAAGACTGAATTG 672

## RESULT 7

US-10-243-402-27  
; Sequence 27, Application US/10243402  
; Publication No. US20030138902A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C39  
; CURRENT APPLICATION NUMBER: US/10/243,402  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 27  
; LENGTH: 920  
; TYPE: DNA  
; ORGANISM: Homo Sapien

US-10-243-402-27

Alignment Scores:  
Pred. No.: 1.33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-243-402-27 (1-920)  
Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCCGATCTCTAGCCGCCACTCACA 114  
Qy 21 GlnGlyArgTyrValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
Db 115 CAAGGCGAGTGGGTGAGGAATCCAGAGTTGCCATGGAGAAATTCAGGTGTGAGCATTC 174  
Qy 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACACAGCTCAAAACCTGGAGCC 234  
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTyrGly 80  
Db 235 AAAAAGGACACAAAGGACTCTGACCCAACTGCCCCAGACCTCTCCAGAGGTGGGGT 294  
Qy 81 AspGlnLeuIleTyrThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAGACAGCAAC 354  
Qy 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
Db 355 AAACCTTGTGATGATTATTCATCACTTGGATAGTGGCCACACAGTCAAGCTTTAAAGAAA 414  
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
Db 415 GTGTTTGTCTGAAAATAAAGAAATCCAGAAATTTGGCAGACAGTTCCTCTCCATCTCTG 474  
Qy 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160  
Db 475 GTTATGAAGAACTGACAAACACCTTTCTCTGATGGCCAGTATGTCCCAGATTATG 534  
Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180  
Db 535 TTTGTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAAATCGTCTC 594  
Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLys 200  
Db 595 TATGCTTACGAACCTGCGAGATACAGCTCTGTGTTGTTGACCAACATGAAGAAAGCTCTCAAG 654  
Qy 201 LeuLeuLysThrGluLeu 206  
Db 655 TTGCTGAAGACTGAATTG 672

## RESULT 8

US-10-243-431-27  
; Sequence 27, Application US/10243431  
; Publication No. US20030138903A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C37  
; CURRENT APPLICATION NUMBER: US/10/243,431  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046

```
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 27
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-243-431-27

Alignment Scores:
Pred. No.: 1,33e-130 Length: 920
Score: 1025.00 Matches: 203
Percent Similarity: 98.54% Conservativeness: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 96.43% Indels: 1
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-243-431-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
Db 56 AGACTCAGCTGTGCTGGACACTCAGAGCTT-GGACCCGATCTTAGCCGCGACTCACA 114

QY 21 GlnGlyArgTTPValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
Db 115 CAAGCAGCGTGGTGGAGAAATCCAGAGTTGCCATGGAGAAATCCAGTGTCCAGATTTC 174

QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
Db 175 TTGCTCTTGTGGCCCTCTCTTACACTCTGGCCAGAGATACACAGTCAAACTGGAGCC 234

QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTTPGly 80
Db 235 AAAAGGACAAAGAGCTCTCGACCCAACTGCCCGCCAGACCTCTCCAGAGTTGGGT 294

QY 81 AspGlnLeuIleTTPThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAGACAGCAAC 354

QY 101 LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
Db 355 AAACCCCTTGATGATTATTCATCACTTGGATGAGTCCACACAGTCAAGCTTTAAAGAA 414

QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluInPheValLeuLeuAsnLeu 140
Db 415 GGTGTTGCTGAAATAAAGAAATCAGAAATGGCAGAGCAGTTGTCTCTCTCAATCTG 474

QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
Db 475 GTTTATGAACAACATGACAAACCTTCTCTGATGGCCAGTATGTCCTCCAGGATTATG 534

QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
Db 535 TTTGTTGACCCATCTCTGACAGTTCAGAGCCGATATCACTGGAAGATATTAATCGTCTC 594

QY 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
Db 595 TATGCTTACGAACCTGCGAGATACAGCTCTGTGTTGCTTGACAAATCAATGAAGAAAGCTCTCAAG 654

QY 201 LeuLeuLysThrGluLeu 206
Db 655 TTGCTGAAGACTGAATTG 672

RESULT 9
US-10-245-164-27
; Sequence 27, Application US/10245164
; Publication No. US20030138904A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C76
; CURRENT APPLICATION NUMBER: US/10/245,164
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 27
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-164-27

Alignment Scores:
Pred. No.: 1,33e-130 Length: 920
Score: 1025.00 Matches: 203
Percent Similarity: 98.54% Conservativeness: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 96.43% Indels: 1
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-245-164-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
Db 56 AGACTCAGCTGTGCTGGACACTCAGAGCTT-GGACCCGATCTTAGCCGCGACTCACA 114

QY 21 GlnGlyArgTTPValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
Db 115 CAAGCAGCGTGGTGGAGAAATCCAGAGTTGCCATGGAGAAATCCAGTGTCCAGATTTC 174

QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
```

Db 175 TTGCTCTTGGCCCTCTCTACACTCTGGCCAGAGATACCACAGTCAACCTGGAGCC 234  
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
Db 235 AAAAAGGACAAAGGACTCTCGACCCAAATGCCCCAGACCCCTCTCCAGAGGTGGGGT 294  
Qy 81 AspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAGACAAGCAAC 354  
Qy 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
Db 355 AAACCCCTTGATGATTATTCATCACTTGGATGAGTGGCCACACAGTCAAGCTTTAAAGAAA 414  
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
Db 415 GTGTTTGTCTGAAAATAAAGAAATCCAGAAATGGCAGAGCAGTTTGTCTCTCAATCTG 474  
Qy 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160  
Db 475 GTTTATGAACAACTGACAAACACCTTCTCTCTGATGGCCAGATATGCCCCAGGATTATG 534  
Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180  
Db 535 TTGTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAGATATTCAAATCGTCTC 594  
Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200  
Db 595 TATGCTTACGAACCTGCAGATACAGCTCTGTGCTTGACAAACATGAAGAAAGCTCTCAAG 654  
Qy 201 LeuLeuLysThrGluLeu 206  
Db 655 TTGCTGAAGACTGAATTG 672

## RESULT 10

US-10-244-972-27  
; Sequence 27, Application US/10244972  
; Publication No. US20030170809A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C75  
; CURRENT APPLICATION NUMBER: US/10/244,972  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 27  
; LENGTH: 920  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-244-972-27  
Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0  
US-09-674-266A-181 (1-206) x US-10-244-972-27 (1-920)  
Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTTAGCCGCCGACTCACA 114  
Qy 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
Db 115 CAAGGAGGTTGGGTGAGGAAATCCAGAGTTGCCATGGAGAAATTCAGTGTCCAGCATTC 174  
Qy 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyVala 60  
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACACAGTCAAACTCGAGCC 234  
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
Db 235 AAAAAGGACAAAGGACTCTCGACCCAAATGCCCCAGACCCCTCTCCAGAGGTGGGGT 294  
Qy 81 AspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAGACAAGCAAC 354  
Qy 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
Db 355 AAACCCCTTGATGATTATTCATCACTTGGATGAGTGGCCACACAGTCAAGCTTTAAAGAAA 414  
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
Db 415 GTGTTTGTCTGAAAATAAAGAAATCCAGAAATGGCAGAGCAGTTTGTCTCTCAATCTG 474  
Qy 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160  
Db 475 GTTTATGAACAACTGACAAACACCTTCTCTCTGATGGCCAGATATGCCCCAGGATTATG 534  
Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180  
Db 535 TTGTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTC 594  
Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200  
Db 595 TATGCTTACGAACCTGCAGATACAGCTCTGTGCTTGACAAACATGAAGAAAGCTCTCAAG 654  
Qy 201 LeuLeuLysThrGluLeu 206  
Db 655 TTGCTGAAGACTGAATTG 672  
RESULT 11  
US-10-197-942-27  
; Sequence 27, Application US/10197942  
; Publication No. US20030175862A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan

APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C1(US)  
CURRENT APPLICATION NUMBER: US/10/197,942  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091358  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/106932  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/115554  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119342  
PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/123957  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123972  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: 60/127372  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/131271  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/133459  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/135725  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/135729  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/135750  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/138385  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/140653  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/141037  
PRIOR FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: 60/144732  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/144758  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/144790  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145228  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 60/146222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 60/146843  
PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/148188  
PRIOR FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: 60/148513  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 60/149327  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149395  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/150114  
PRIOR FILING DATE: 1999-08-20  
PRIOR APPLICATION NUMBER: 60/151700  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/151734  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/162506  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 60/170262  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/177118  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: 60/179851  
PRIOR FILING DATE: 2000-02-02  
PRIOR APPLICATION NUMBER: 60/180921  
PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 60/187202  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/198587  
PRIOR FILING DATE: 2000-04-18  
PRIOR APPLICATION NUMBER: 60/199614  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 60/206330  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/206368  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/209832  
PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: 60/218371  
PRIOR FILING DATE: 2000-07-13  
PRIOR APPLICATION NUMBER: 60/222695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/229896  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/230621  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/232887  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/235147  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/261878  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 60/261910  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/261939  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/262150  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/264395  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/266421  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 60/267623  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/274399  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/280982

; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/282129  
 ; PRIOR FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: 60/282199  
 ; PRIOR FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: 60/290589  
 ; PRIOR FILING DATE: 2001-05-09  
 ; PRIOR APPLICATION NUMBER: 09/180997  
 ; PRIOR FILING DATE: 1998-11-19  
 ; PRIOR APPLICATION NUMBER: 09/267213  
 ; PRIOR FILING DATE: 1999-03-12  
 ; PRIOR APPLICATION NUMBER: 09/380137  
 ; PRIOR FILING DATE: 1999-08-25  
 ; PRIOR APPLICATION NUMBER: 09/380138  
 ; PRIOR FILING DATE: 1999-08-25  
 ; PRIOR APPLICATION NUMBER: 09/403297  
 ; PRIOR FILING DATE: 1999-10-18  
 ; PRIOR APPLICATION NUMBER: 09/423741  
 ; PRIOR FILING DATE: 1999-11-10  
 ; PRIOR APPLICATION NUMBER: 09/709238  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: 09/802706  
 ; PRIOR FILING DATE: 2001-03-09  
 ; PRIOR APPLICATION NUMBER: 09/872035  
 ; PRIOR FILING DATE: 2001-06-01  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 09/924419  
 ; PRIOR FILING DATE: 2001-08-06  
 ; PRIOR APPLICATION NUMBER: 09/927796  
 ; PRIOR FILING DATE: 2001-08-09  
 ; PRIOR APPLICATION NUMBER: 09/929404  
 ; PRIOR FILING DATE: 2001-08-13  
 ; PRIOR APPLICATION NUMBER: 09/931836  
 ; PRIOR FILING DATE: 2001-08-16  
 ; PRIOR APPLICATION NUMBER: 09/941992  
 ; PRIOR FILING DATE: 2001-08-28  
 ; PRIOR APPLICATION NUMBER: 09/946374  
 ; PRIOR FILING DATE: 2001-09-04  
 ; PRIOR APPLICATION NUMBER: 10/001054  
 ; PRIOR FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: 10/052586  
 ; PRIOR FILING DATE: 2002-01-15  
 ; PRIOR APPLICATION NUMBER: 10/081056  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: 10/119480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: PCT/US98/18824  
 ; PRIOR FILING DATE: 1998-09-10

Alignment Scores:  
 Pred. No.: 1 33e-130 Length: 920  
 Score: 1025.00 Matches: 203  
 Percent Similarity: 98.54% Conservative: 0  
 Best Local Similarity: 98.54% Mismatches: 3  
 Query Match: 96.43% Indels: 1  
 DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-197-942-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgLeuThr 20  
 Db 56 AGACTCAGCTGTGCTGGCACACTCAGAGCTT-GGACCGCATCTTAGCGCGGACTCACA 114  
 Qy 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
 Db 115 CAAGCGAGGTGGGTGAGGAAATCCAGAGTTGCGCATGGAGAAATTCAGAGTGTCCAGCATTC 174  
 Qy 41 LeuLeuLeuValAlaLeuSerTrpThrLeuAlaArgAspThrThrValLysProGlyVala 60  
 Db 175 TTGCTCTTGTGGCCCTCTCCCTACTCTGCGCAGATACACAGTCAACACCTGGAGCC 234  
 Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLysSerArgGlyTrpGly 80

Db 235 AAAAAGGACACAAAGGACTCTCGACCCAACTGCCAGACCCCTCTCCAGAGGTTGGGGT 294  
 Qy 81 AspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
 Db 295 GACCAACTCATCTGGACTCAGACATATGAGAGCTCTATATAAATCCACAGCAAC 354  
 Qy 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
 Db 355 AAACCCCTTGATGATTATTTCATCCTTGGATGAGTGGCCACAGCTCAAGCTTTAAAGAAA 414  
 Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
 Db 415 GTGTTTGCTGAAAAATAAGAAATCCAGAAATGGCAGACAGTTGTCTCTCTCAATCTG 474  
 Qy 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160  
 Db 475 GTTATGAACAACACTGACAAACACCTTTCTCTGATGGCCAGTATGTCCTCCAGATTATG 534  
 Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180  
 Db 535 TTTGTTGACCCATCTCTGACAGTTAGACGATACAGTCTGTGTGTTGACATGAAAGAACTCTCAAG 654  
 Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuAspAsnMetLysLysAlaLeuLys 200  
 Db 595 TATGCTTACGAACCTGCGAGATACAGTCTGTGTGTTGACATGAAAGAACTCTCAAG 654  
 Qy 201 LeuLeuLysThrGluLeu 206  
 Db 655 TTGCTGAAGACTGAATTG 672

RESULT 12  
 US-10-238-196-27  
 ; Sequence 27, Application US/10238196  
 ; Publication No. US20030186372A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Phillippe  
 ; APPLICANT: Watanbe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Fong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3630R1C8  
 ; CURRENT APPLICATION NUMBER: US/10/238,196  
 ; CURRENT FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 10/197942  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/059114  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/063046  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/065027  
 ; PRIOR FILING DATE: 1997-11-10  
 ; PRIOR APPLICATION NUMBER: 60/079689  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/086478  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/089801  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/090557  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090689  
 ; PRIOR FILING DATE: 1998-06-25

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 27

; LENGTH: 920

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-238-196-27

Alignment Scores:

Pred. No.: 1.33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservatives: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-238-196-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgLeuThr 20  
|||  
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTAGCCGCGACTCACA 114  
|||  
QY 21 GlnGlyArgTyrValArgLysSerArgValAlaMetGluLysIleProValSerAla 40  
|||  
Db 115 CAAGGAGGTGGTGGAGAAATCCAGAGTGGCATGGAGAAATCCAGTGTCCAGTTC 174  
|||  
QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
|||  
Db 175 TTGCTCTTGTGGCTCTCTACACTCTGGCCAGAGATACACAGTCAAACTGGAGCC 234  
|||  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTyrGly 80  
|||  
Db 235 AAAAAGGACACAAAGACTCTCGACCCAACTGCCCGACCTCTCCAGAGTGGGT 294  
|||  
QY 81 AspGlnLeuIleTyrThrClnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
|||  
Db 295 GACCAACTCATCTGACACTCAGACATATGAAGAAGCTCTATATAAATCCAAAGCAAC 354  
|||  
QY 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
|||  
Db 355 AAACCTTGATGATTATTCATCATCTGATGATGAGTGGCCACAGTCAAGCTTTAAAGAA 414  
|||  
QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
|||  
Db 415 GTGTTTGTGTAATAAAGAAATCCAGAAATGGCAGAGCACTTTGTCTCTCAATCTG 474  
|||  
QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160  
|||  
Db 475 GTTATGAACAACACTGACAAACACCTTTCTCTGTATGGCCAGTATGTCCCGAGATTATG 534  
|||  
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyr-SerAsnArgLeu 180  
|||  
Db 535 TTGTTGACCCATCTCTGACAGTTAGCCGATATACCTGGAAGATATTCATTCCTC 594  
|||  
QY 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200  
|||  
Db 595 TATGCTTACGAACCTCGAGATACAGCTCTGTTGCTTGACCAACATGAAGAAGCTCTCAAG 654  
|||  
QY 201 LeuLeuLysThrGluLeu 206  
|||  
Db 655 TTGCTGAAGACTGAATTG 672  
|||

RESULT 13

US-10-245-013-27

; Sequence 27, Application US/10245013

; Publication No. US20030186373A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Eaton, Dan

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Goddard, Audrey

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Phillippe

; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P363081C96

; CURRENT FILING DATE: 2002-09-16

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/063046

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/065027

; PRIOR FILING DATE: 1997-11-10

; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/086478

; PRIOR FILING DATE: 1998-05-22

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/089801

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/090557

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: 60/090689

; PRIOR FILING DATE: 1998-06-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 27

; LENGTH: 920

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-245-013-27

Alignment Scores:

Pred. No.: 1.33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservatives: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-245-013-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
|||  
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTAGCCGCGACTCACA 114  
|||  
QY 21 GlnGlyArgTyrValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
|||  
Db 115 CAAGCAGGTGGTGGAGAAATCCAGAGTTCCTCATGGAGAAATTCAGTGTCCAGTTC 174  
|||  
QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
|||  
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGCCAGAGATACACAGTCAAACTGGAGCC 234  
|||  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTyrGly 80  
|||  
Db 235 AAAAAGGACACAAAGGACTCTCGACCCAACTGCCCGACCTCTCCAGAGTGGGT 294  
|||  
QY 81 AspGlnLeuIleTyrThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
|||  
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAAGCAAC 354  
|||  
QY 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
|||  
Db 355 AAACCTTGATGATTATTCATCATCTGATGATGAGTGGCCACAGTCAAGCTTTAAAGAA 414  
|||

Qy	121	ValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGluInPheValLeuLeuAsnLeu	140
Db	415	GTGTTTGCTGAAAAATAAAGAAATCCAGAAATTTGCAGAGCAGATTTGTCTCTCCCTCAATCTG	474
Qy	141	ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgGlleMet	160
Db	475	GTTTATGAAACAACTCGACAAACACTTCTCTCTGATGGCCAGTATGTGCCCAGGANTATG	534
Qy	161	PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu	180
Db	535	TTTGTGTGCCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTC	594
Qy	181	TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys	200
Db	595	TATGCTTACGAACCTCGCAGATACAGCTCTGTTGCTTGACACACATGAAGAAAGCTCTCAAG	654
Qy	201	LeuLeuLysThrGluLeu	206
Db	655	TTTGCTGAAGACTGAATTG	672

## RESULT 14

```

US-10-245-103-27
/ Sequence 27, Application US/10245103
/ Publication No. US20030068778A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3630R1C112
/ CURRENT APPLICATION NUMBER: US/10/245,103
/ CURRENT FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 27
/ LENGTH: 920
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-245-103-27

```

Alignment Scores:	
Pred. No.:	1.33e-130
Score:	1025.00
Length:	920
Matches:	203

Percent Similarity:	98.54%	Conservative:	0
Best Local Similarity:	98.54%	Mismatches:	3
Query Match:	96.43%	Indels:	1
DB:	14	Gaps:	0
US-09-674-266A-181 (1-206) x US-10-245-103-27 (1-920)			
Qy	1	ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr	20
Db	56	AGACTCAGCTGTGTGGCACACTCAGAAAGCTT-GGACCGCATCTCTAGCGCGCACTCACA	114
Qy	21	GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysValIleProValSerAlaPhe	40
Db	115	CAAGCGAGGTGGTGAGAAATCCAGAGTTCCTCGAGGAGAAATTCAGAGTGTCCAGATTC	174
Qy	41	LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla	60
Db	175	TTGCTCTTGTGGCCCTCTCTCACACTCTGGCCAGAGATACCACAGTCAAACTCGAGCC	234
Qy	61	LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly	80
Db	235	AAAAGAGACAAAGGACTCTCGACCCAAACTGCCCCAGACCCCTCTCCAGAGGTTGGGGT	294
Qy	81	AspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn	100
Db	295	GACCACTCATCTGCACTCAGACATATGAAGAGCTCTATATAATCCNAGACACAGCAAC	354
Qy	101	LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys	120
Db	355	AAACCTTGATGATTATTTCATCACTTGGATGAGTGCCACACAGTCAAGCTTTAAAGAAA	414
Qy	121	ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu	140
Db	415	GTGPTTCTGAAAAATAAGAAATCCAGAAATGGCAGACAGCTTTGTCTCTCTCAATCTG	474
Qy	141	ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet	160
Db	475	GTTTATGAAACAACGTGACAAACACCTTTCTCTGATGCCAGTATGTCCTCCAGGATTATG	534
Qy	161	PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu	180
Db	535	TTTGTTCACCCATCTCTGACAGTTAGACGCCGATATCATCTGGAAGATATTTCAAATCGTCTC	594
Qy	181	TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys	200
Db	595	TATGCTTACGNACCTGCAGATACAGCTCTGTGTGTTGACACATCATGAGBAAGCTCTCAAG	654
Qy	201	LeuLeuLysThrGluLeu	206
Db	655	TTGCTGAAGACTGAATTG	672

RESULT 15

```

RES001 13
US-10-245-107-27
; Sequence 27, Application US/10245107
; Publication No. US20030068779A1
;
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630RIC71
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16

```



;; PRIOR APPLICATION NUMBER: 10/197942  
;; PRIOR FILING DATE: 2002-07-18  
;; PRIOR APPLICATION NUMBER: 60/059114  
;; PRIOR FILING DATE: 1997-09-17  
;; PRIOR APPLICATION NUMBER: 60/063046  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/065027  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 60/079689  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/086478  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090689  
;; PRIOR FILING DATE: 1998-06-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 116  
;; SEQ ID NO 27  
;; LENGTH: 920  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-245-107-27

Alignment Scores:  
Pred. No.: 1.33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 14 Gaps: 0

US-09-674-266a-181 (1-206) x US-10-245-107-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
DB 56 AGACTCAGCTGTGCTGGACACTCAGAACCTT-GGACCCGATCCTAGCCGCGACTCACA 114  
QY 21 GlnGlyArgTyrValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
DB 115 CAAGCAGCTGGGTGAGGAATCCAGAGTTGCCATGGAGAAATTCACGTGTCCAGATTC 174  
QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
DB 175 TTGCTCCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACCACAGTCAAACTGGAGCC 234  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTyrGly 80  
DB 235 AAAAAGGACAAAGAGACTCTCGACCCAACTGCCCCAGACCCCTCTCCAGAGGTGGGGT 294  
QY 81 AspGlnLeuIleTyrThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
DB 295 GACCAACTCTCTGGACTCAGACATATGAAGAGCTCTATATAATCCAGACAGCAAC 354  
QY 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
DB 355 AAACCCCTTCATGATTATTCATCATTGGATGAGTGCCACACAGTCAAGCTTTAAAGAA 414  
QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
DB 415 GTGTTTGCTGGAATAAAGAAATCCAGAAATGGCAGAGCAGTTGTCTCTCTCAATCTG 474  
QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160  
DB 475 GTTTATGAACAACACTGACAAACACCTTTCTCTGATGGCCAGTATGTCCCCAGGATTATG 534  
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180  
DB 535 TTTGTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAGATATTCAAAATCGTCTC 594

QY 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200  
DB 595 TATGCTTACGAACCTGCAGATACAGCTCTGTGCTTGACACATGAGAAAGCTCTCAAG 654  
QY 201 LeuLeuLysThrGluLeu 206  
DB 655 TTGCTGAAGACTGAATTG 672

Search completed: November 30, 2003, 05:00:53  
Job time : 311 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2003, 15:52:53 ; Search time 21 Seconds  
(without alignments)  
943.369 Million cell updates/sec

Title: US-09-674-266A-181  
Perfect score: 1063  
Sequence: 1 RLSCAGTSLSGGPHPSRLT.....DTALLDNMKALKLKTTEL 206

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	899	84.6	175	JE0350	Anterior gradient-
2	199	18.7	186	T31643	hypothetical prote
3	119	11.2	150	D63100	probable protein d
4	87.5	8.2	458	S50919	hypothetical prote
5	87	8.2	348	G72016	probable disulfide
6	87	8.2	348	C86607	disulfide bond iso
7	85.5	8.0	1830	S19188	myosin-V - chicken
8	84.5	7.9	1151	AG1717	probable peptidogl
9	84	7.9	771	S51421	hypothetical prote
10	83.5	7.9	217	T37859	probable transcrip
11	83.5	7.9	918	C96829	unknown protein F1
12	83	7.8	479	T40683	cell cycle protein
13	83	7.8	507	S56143	cell cycle protein
14	82.5	7.8	788	C70441	lipote-protein li
15	81.5	7.7	893	GS9431	phosphatidylinosit
16	81.5	7.7	970	S29069	inositol polyphosp
17	81.5	7.7	1158	T50454	probable rho1 Gp-
18	81.5	7.7	1397	T10466	DNA topoisomerase
19	81	7.6	610	T22909	hypothetical prote
20	81	7.6	635	T23874	hypothetical prote
21	80	7.5	154	F82633	probable protein d
22	80	7.5	259	A96740	F14023.14 [impor
23	80	7.5	847	S53947	hypothetical prote
24	79.5	7.5	277	T37629	hypothetical prote
25	79.5	7.5	301	G71929	GTP-binding protei
26	79.5	7.5	642	F83718	ABC transporter (A
27	79.5	7.5	921	F84593	hypothetical prote
28	79	7.4	477	T37791	probable rna polym
29	79	7.4	510	S43516	carboxypeptidase C

30 78.5 7.4 280 2 A69590 shikimate 5-dehydr  
31 78.5 7.4 917 2 T05430 hypothetical prote  
32 78.5 7.4 1033 2 A96714 hypothetical prote  
33 78.5 7.4 1262 2 I48855 tripeptidyl-peptid  
34 78.5 7.4 1570 2 AC2012 hypothetical prote  
35 78 7.3 337 2 S06956 segmentation prote  
36 78 7.3 1828 2 B59254 myosin heavy chain  
37 78 7.3 1853 1 A46761 myosin heavy chain  
38 78 7.3 1855 2 A59254 myosin heavy chain  
39 76.5 7.2 985 2 E59850 formate dehydrogen  
40 76.5 7.2 1025 2 T10259 RNA-directed DNA p  
41 76 7.1 166 2 E2018 thioredoxin disulf  
42 76 7.1 166 2 D86606 thioredoxin disulf  
43 76 7.1 367 2 T39574 oligopeptide-bindi  
44 76 7.1 543 1 F64871 probable peptide A  
45 76 7.1 583 2 E75529

ALIGNMENTS

RESULT 1

JE0350  
Anterior gradient-2 - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: JE0350  
R:Thompson, D.A.; Weigel, R.J.  
Biochem. Biophys. Res. Commun. 251, 111-116, 1998  
A:Title: hAG-2, the human homologue of the Xenopus laevis cement gland gene XAG-2, is c  
A:Reference number: JE0350; MUID:99009231; PMID:9790916  
A:Accession: JE0350  
A:Molecule type: mRNA  
A:Residues: 1-175 <THO>  
A:Cross-references: GB:AF007791; NID:g3779196; PIDN:AAC77358.1; PID:g3779197  
C:Comment: This protein is coexpressed with estrogen receptor (ER) in breast cancer cell  
C:Genetics:  
A:Gene: hAG-2  
C:Superfamily: human anterior gradient-2

Query Match 84.6%; Score 899; DB 2; Length 175;  
Best Local Similarity 100.0%; Pred. No. 3.1e-74;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQYEE 91  
Db 1 MEKIPVSFLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQYEE 60  
QY 92 ALYKSKTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSKTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSP 120  
QY 152 DGQVPRIMFVDPSTLVRADITGRYSNRLYAYEPADTALLDNMKALKLKTTEL 206  
Db 121 DGQVPRIMFVDPSTLVRADITGRYSNRLYAYEPADTALLDNMKALKLKTTEL 175

RESULT 2

T31643  
hypothetical protein Y57A10A.u - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T31643  
R:Smyle, R.  
submitted to the EMBL Data Library, September 1999  
A:Reference number: Z21048  
A:Accession: T31643  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-186 <WIL>  
A:Cross-references: EMBL:AL117195; PIDN:CAB55026.1; CESP:Y57A10A.u  
A:Experimental source: clone Y57A10A  
C:Genetics:

A;Gene: CESP:Y57A10A.u  
A;Introns: 70/1  
C;Superfamily: human anterior gradient-2

Query Match 18.7%; Score 199; DB 2; Length 186;  
Best Local Similarity 30.0%; Pred. No. 1.1e-10;  
Matches 51; Conservative 38; Mismatches 57; Indels 24; Gaps 6;

QY 41 LLLVALSYTLARDTTVPKAGKDTKSRPKLPQTLSRGWDQLIWTQTYEALYKSKTSN 100

Db 4 LLLAL-----VSASAYASPDKTKDSIQNPLARGFGDDIAWVK-WEDATETALDTD 53

QY 101 KPLMIHHLDECPHSQALKVFAEN---KEIQKLAQFVLLNLV--YETTDKHLSPDQY 155

Db 54 KPFLHLHKSCHACKALKTKTFOGNAKAKFKLSEHFVWVNTEDDDPEPEEYRPDCKY 113

QY 156 VPRIMFVDPSTVRADITGRYSNRL-----YAYEPADTALLDNMKALK 200

Db 114 IPRLLFLDKN---GDLLEQFKNKAEYKKNYAYVYSSPADILNSMKDVLK 159

RESULT 3  
D69100  
probable protein disulfide-isomerase (EC 5.3.4.1) MTH1745 [similarity] - Methanobacterium  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Sep-2000  
C;Accession: D69100

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funch

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: D69100

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-150 <MTH>

A;Cross-references: GB:AE000930; GB:AE000666; NID:g2622872; PIDN:AA886215.1; PID:g262287

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH1745

C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 11.28; Score 119; DB 2; Length 150;

Best Local Similarity 27.1%; Pred. No. 0.0015;

Matches 35; Conservative 28; Mismatches 46; Indels 20; Gaps 4;

QY 39 AFLLLVALSYTLARDTTVPKAGKDTKDSRPKLPQTLSRGWDQLIWTQTYEALYKSKT 98

Db 19 AGLSLVLIITV-----QPRVPSLTDEKD-LKWYTEHDEAIKEASR 60

QY 99 SNKPLMIHHLDECPHSQALKVFAENKEIQ-KLAQFVLLNLVYETTDKHLSPDQY-V 156

Db 61 TGNVNFVFSASWCPACQKLESETLQNTVEQRLAEDFIAVKIDVDTSPALSSRYIYGV 120

QY 157 PRIMFVDP 165

Db 121 PTVIIDPS 129

RESULT 4  
S50919  
hypothetical protein YMR191w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YW9646.03

A;Cross-references: EMBL:Z47815; NID:g642280; PIDN:CAA87812.1; PID:g642283; MIPS:YMR191w  
R;Gangloff, S.; McDonald, J.P.; Bendixen, C.; Arthur, L.; Rothstein, R.  
Mol. Cell. Biol. 14, 8391-8398, 1994

A;Title: The yeast type I topoisomerase Top3 interacts with Sgs1, a DNA helicase homolog

A;Reference number: A56359; MUID:95059068; PMID:7969174

A;Accession: S55721

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-127, 'Y', 129-131, 'LALG', 136-249 <CAN>

A;Cross-references: EMBL:U22341; NID:g726277; PIDN:AB60288.1; PID:g726278

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995

C;Genetics:

A;Map position: 13R

A;Superfamily: Saccharomyces cerevisiae hypothetical protein YMR191w

Query Match 8.2%; Score 87.5; DB 2; Length 458;

Best Local Similarity 20.1%; Pred. No. 4.5;

Matches 55; Conservative 35; Mismatches 74; Indels 109; Gaps 13;

QY 15 PSRLTQGG-----RWYKSRVAMEKIPVSAFLLLVALS----- 47

Db 82 PTERMAVGGNNWSMWRGMRVHLRQITKSLDRTLSLSHGNSFHSQYNNRNFTVWTKSLFE 141

QY 48 -----YTLARDTTVPKAGKDTK-----DSRPKLPQTLSRG---W---GD 81

Db 142 ASTAFRRASGLTVSPLTRGCIARFDFHFRPVNVYKFSASPRVPKAGPGLFTNNMTTSK 201

QY 82 QLIWTQTYEALYK---SKTSNKPLMI-----IHLDECPHSQ--- 116

Db 202 RLLGQRAYSTSSIKFTQEVANNMTISLRGFFNSLGLGNCSSNSKAYQNASNVTSKQD 261

QY 117 -----ALKKV-----FAENKEIQKLAQFVLLNLVYETTDKHLSPDQYV----- 156

Db 262 HVQPVALKKQSKQDINFIRNLKFKMK--TQNEVVDTSAYIMKPGSYIEFTISFNV 319

QY 157 -----PRIMFVDPSTVRADITGRYSNRLYAYE 184

Db 320 NGTFSAPLFLDPSLL--ADLDEMIRN--YKYE 348

RESULT 5  
G72016

probable disulfide bond isomerase - Chlamydia pneumoniae (strains CWL029 and AR39)

C;Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000

C;Accession: G72016; B81523

R;Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: G72016

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-348 <ARN>

A;Cross-references: GB:AE001673; GB:AE001363; NID:g4377252; PIDN:AAD19071.1; PID:g437725

A;Experimental source: strain CWL029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.;

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: B81523

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-348 <REA>

A;Cross-references: GB:AE002251; GB:AE002161; NID:g7189833; PIDN:AAF38711.1; PID:g7189840

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CPN0933; CP0928

Query Match 8.2%; Score 87; DB 2; Length 348;

Best Local Similarity 25.0%; Pred. No. 3.5;

```

A;Title: cDNA encoding the chicken ortholog of the mouse dilute gene product. Sequence
A;Reference number: S29249; MUID:93012002; PMID:1383040
A;Accession: S29249
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1142, 1144-1830 <S>AN>
A;Cross-references: EMBL:X67251; NID:G63364; PIDN:CAA47673.1; PID:G63365
C;Comment: The neck domain comprises six approximately 23-residue tandem repeats; this
C;Superfamily: myosin MYO2; myosin motor domain homology
C;Keywords: actin binding; ATP; brain; coiled coil; nucleotide binding; P-loop; phospho;
F;72-752/Domain: myosin motor domain homology <MMOT>
F;163-170/Region: nucleotide-binding motif A (P-loop)
F;645-666/Region: actin binding #status predicted
F;765-909/Domain: neck #status predicted <NEC>
F;912-1420/Domain: coiled coil #status predicted <COI>
F;1421-1830/Domain: carboxyl-terminal domain #status predicted <CTD>
F;169/Binding site: ATP (Lys) #status predicted
F;1735/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match      8.0%; Score 85.5; DB 1; Length 1830;
Best Local Similarity 28.1%; Pred. No. 38;
Matches 27; Conservative 21; Mismatches 41; Indels 7; Gaps 3;

Qy      63  DTKDSRPKLQPTLSRCGQDGLIWTQTYEALY-KSKTSNKLPMI IHHLDECPH--SQALK 119
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      507 DLDDECKMPKGGDDTWAQKLNYNHLNKALCEKPLSNKAFIIRKFADKVEYQCSGFLE 566
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      120 K-----VFAENKEIQKLAEQFVLINLVYETTTDKHLSP 151
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

567 KNAQIVIEERQIKVLRSSKRAKLLDFELFQDEERKALSP 602

DD

RESULT 8

AG1717

probable peptidoglycan bound protein (LPXTG motif) lin2283 [imported] - *Listeria innocua*

C;Species: *Listeria innocua*

C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001

C;Accession: AG1717

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke, J.; Dominguez-Bernal, G.; Duchaud, L.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Authors: Kreitt, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maqueno, E.; Maitournam, A.; M...  
A:Title: Comparative genomics of *Listeria species*.  
A:Reference number: AB1077; MUID: 21537279; PMID: 11679669  
A:Accession: AG1717  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1151 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC97511.1; PID:g16414795; GSPDB:GN00178  
A:Experimental source: strain Cl1p11262  
C:Genetics:  
A:Gene: lin2283

Query Match 7.9%; Score 84.5; DB 2; Length 1151;  
Best Local Similarity 22.8%; Pred. No.26;  
Matches 44; Conservative 31; Mismatches 51; Indels 67; Gaps 10;

Qy 50 LARDTTVKFGAKK--DTKDSRKLPTQLSRGQDQLITQ-----Tye 90  
db 961 VALDDSVAPVTVQYVDNHHKQIASPETLTGAGYKFTAKOKKITTNTLVKTPANVSGETN 1020

[illegible]

Db 1112 ADVNKSAPLQPT 1124

RESULT 9

S51421

hypothetical protein YLR176c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L9470.18

C:Species: Saccharomyces cerevisiae

C>Date: 23-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 06-Feb-1998

C:Accession: S51421

R:Wohldmann, P.

submitted to the EMBL Data Library, November 1994

A:Description: The sequence of *S. cerevisiae* cosmid 9470.

A:Reference number: S51414

A:Accession: S51421

A:Molecule type: DNA

A:Residues: 1-771 <WOH>

A:Cross-references: EMBL:U17246; NID:9577192; PID:9577210; MIPS:YLR176C

C:Genetics:

A:Gene: SGD:RFX1

A:Cross-references: SGD:S0004166; MIPS:YLR176C

A:Map position: 12R

Query Match 7.9%; Score 84; DB 2; Length 771;

Best Local Similarity 25.7%; Pred. No. 18;

Matches 47; Conservative 29; Mismatches 67; Indels 40; Gaps 8;

Qy 8 LSGSGP-----HPSRLTQGR-----WVRKSRVAMEKIPVSAFLLLVALSYTLAR 52

Db 89 LIGSGPGSHKPSPTPTOPPAQATQROPATYSVYPASISLNRSSAYPLSFKEETLNN 148

Qy 53 D--TTVK-----PGAKTKDSRPKLPOTLSRGWDQLIWTQTYEALYKSKTSNKP 102

Db 149 NPPTAARTNTPSPISSTKQKTSQKRISSTSRNTQETIAKQIAEN--NKSRTIEY 206

Qy 103 LMIITH-----LDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSPDQGY 155

Db 207 AQIVKHAIEKVLMSDQNTSKAALQAEQNRER--QVFALLWMKNCKSQHDS----Y 260

Qy 156 VPR 158

Db 261 VPR 263

RESULT 10

T37859

probable transcription factor - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: T37859

R:Davidin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z21750

A:Accession: T37859

A:Status: preliminary;

A:Molecule type: DNA

A:Residues: 1-217 <DEV>

A:Cross-references: EMBL:Z69795; PIDN:CAA93690.1; GSPDB:GN00066; SPDB:SPAC1768.07

A:Experimental source: strain 972h-; cosmid c1768

C:Genetics:

A:Gene: SPDB:SPAC1768.07

A:Map position: 1

Query Match 7.9%; Score 83.5; DB 2; Length 217;

Best Local Similarity 20.6%; Pred. No. 4.1;

Matches 42; Conservative 33; Mismatches 80; Indels 49; Gaps 8;

Qy 14 HPSRLTQG-----BWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKD 66

Db 39 HTWKIFVEGVGDGDIKWRK-----VVPKL-----HPTYNPNP---TTTIE 76

Qy 67 SRPKLPOTLSRGWDQLIWTQTYEALYKSKTSNKPMLIIHLDCEPHSQALKKVFAN 126

Db 1112 ADVNKSAPLQPT 1124

Db 77 SPPF--EVIETGWGEFDIMVRIF-----FAPEAHEKALTYFHHKLHPYGPMBEMKASGG 130

Qy 127 EIQLAEQFVLLNLVYETTDKHLSP-----DGOVPRIMFVDPSTLRADITGRYSNRLYA 182

Db 131 LVESVQVEIEVFNEPEFTYTKLSQNPIGDGH-----GLAVESEDPHFPFQOQLEQ 180

Qy 183 YEPADTALLDNNMKKALKLKLKTEL 206

Db 181 DEADKLDFAIQEVKVTIEMKQVQV 204

RESULT 11

C96829

unknown protein F19K16.21 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: C96829

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: C96829

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-918 <STO>

A:Cross-references: GB:AE005173; NID:96453864; PIDN:AAF09048.1; GSPDB:GN00141

C:Genetics:

A:Gene: F19K16.21

A:Map position: 1

Query Match 7.9%; Score 83.5; DB 2; Length 918;

Best Local Similarity 21.3%; Pred. No. 24;

Matches 46; Conservative 41; Mismatches 76; Indels 53; Gaps 9;

Qy 36 PVSAFLLLVALSYTL-----ARDTTVKPGAKKD---TKDSRPKLPOTLSRGWDQLIWT 86

Db 149 PQSQILLLESSEYSLOTPESSGYKTSLOPNKLEMTASQDSQPEQPK--SEASESQPEDS 206

Qy 87 QTYEALYKSKTSNKPML-----IIHLDCEPHSQALKKVFANKEIQKLAEOQVLL--- 138

Db 207 EAKEVTVENKDTVHSPVLDQCHKITTYMETTNEQ---EILGENLEGRSTSKNFEVSPDIN 263

Qy 139 -----NLVYETTDKHLSPDQGYVPR-----IMFVDPSTLRADI--- 172

Db 264 HVNRIESPVAHPSLIFESDG---SPYESSIPKSSSEISERIVDFVSRIDSLRSLTSEL 320

Qy 173 --TGRYSNRLYAYEPADTALLDNNMKKALKLKLKTEL 206

Db 321 NESQSSSATNVSDSADVILELEKTKKIKLENAL 356

RESULT 12

T40683

cell cycle protein kinase hsk1 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000

C:Accession: T40683

R:Lynte, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.

submitted to the EMBL Data Library, January 1999

A:Reference number: Z21944

A:Accession: T40683

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-479 <LYN>

A:Cross-references: EMBL:AL035263; PIDN:CAB38417.1; GSPDB:GN00067; SPDB:SPBC776.12c

A:Experimental source: strain 972h-; cosmid c776

C:Genetics:  
A:Gene: SPDB:SPBC776.12c  
A:Map position: 2  
A:Introns: 77/1, 92/2, 331/1  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 7.8%; Score 83; DB 2; Length 479;  
Best Local Similarity 22.4%; Pred. No. 12;  
Matches 28; Conservative 24; Mismatches 55; Indels 18; Gaps 5;

QY 83 LIWTQTYEALYKSTSNKP-----LMIHHLDECPHSQALKKVFPAENKEIQKLAQFVLL 138  
DB 352 ILWASGSGASIIYKELRHKPSQERLCLEFLKCLDNCNKRISAE-----EALDHDHFLYL 407

QY 139 -NLVYETTDKHLSPDQGVPRIMFVDPSTLVPRADITGRYSNRLYAY---EPADTALLLDN 194  
DB 408 DNLAYEKDDDTAFDNS-----FGTSPKEDDLTAKHLSHLDLFKQSEETDEPTSLSK 461

QY 195 MKKAL 199  
DB 462 RKRSI 466

RESULT 13  
S56143  
cell cycle protein kinase hsk1 (EC 2.7.1.1) - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 28-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 10-Dec-1999  
C:Accession: S56143; T40682  
R:Maeda, H.; Miyake, T.; Arai, K.  
EMBO J. 14, 3094-3104, 1995  
A:Title: hsk1(+), a Schizosaccharomyces pombe gene related to Saccharomyces cerevisiae C  
A:Reference number: S56143; MUID:95347336; PMID:7621824  
A:Accession: S56143  
A:Molecule type: DNA  
A:Residues: 1-507 <NAS>  
A:Cross-references: GB:D50493; NID:9807845; PIDN:BAA09087.1; PID:d1009722; PID:g807846  
A:Experimental source: strain JY2  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.  
submitted to the EMBL Data Library, January 1999  
A:Reference number: Z1944  
A:Accession: T40682  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-507 <LYN>  
A:Cross-references: EMBL:AL035263; PIDN:CAA22885.1; GSPDB:GN00067; SPDB:SPBC776.12c  
A:Experimental source: strain 972h-; cosmid c776  
C:Genetics:  
A:Gene: hsk1; SPBC776.12c  
A:Map position: 2  
A:Introns: 77/1, 359/1  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
C:Keywords: phosphotransferase; protein kinase  
F:66-404/Domain: protein kinase homology <KIN>

Query Match 7.8%; Score 83; DB 2; Length 507;  
Best Local Similarity 22.4%; Pred. No. 13;  
Matches 28; Conservative 24; Mismatches 55; Indels 18; Gaps 5;

QY 83 LIWTQTYEALYKSTSNKP-----LMIHHLDECPHSQALKKVFPAENKEIQKLAQFVLL 138  
DB 380 ILWASGSGASIIYKELRHKPSQERLCLEFLKCLDNCNKRISAE-----EALDHDHFLYL 435

QY 139 -NLVYETTDKHLSPDQGVPRIMFVDPSTLVPRADITGRYSNRLYAY---EPADTALLLDN 194  
DB 436 DNLAYEKDDDTAFDNS-----FGTSPKEDDLTAKHLSHLDLFKQSEETDEPTSLSK 489

QY 195 MKKAL 199  
DB 490 RKRSI 494

RESULT 14

C70441

lipoate-protein ligase A - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999

C:Accession: C70441

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O.V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: C70441

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-788 &lt;AQF&gt;

A:Cross-references: GB:A5000748; NID:92983960; PIDN:AAC07512.1; PID:g2983965; GB:A500065

A:Experimental source: strain VF5

C:Genetics:

A:Gene: lplA





Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	448	42.1	183	1	XAG_XENLA	P55968 xenopus lae
2	437.5	41.2	185	1	NP77_XENLA	P55969 xenopus lae
3	224.5	21.1	170	1	TL19_MOUSE	O9C9U0 mus musculus
4	222	20.9	172	1	TL19_HUMAN	O9S881 homo sapien
5	87.5	8.2	458	1	YMS1_YEAST	P42933 saccharomyce
6	85.5	8.0	1829	1	MYSA_CHICK	O02440 gallus gall
7	84	7.9	811	1	RFX1_YEAST	P48743 saccharomyc
8	83.5	7.9	217	1	YD67_SCHPO	Q10319 schizosacch
9	83	7.8	507	1	HSK1_SCHPO	P50582 schizosacch
10	81.5	7.7	901	1	OCRL_HUMAN	Q01368 homo sapien
11	81.5	7.7	1398	1	TOF2_PLAIFK	P41001 plasmodium
12	80	7.5	339	1	YTH6_RHOER	P43484 rhodococcus
13	80	7.5	843	1	YMG1_YEAST	Q05050 saccharomyc
14	79.5	7.5	301	1	ERA_HELPJ	Q021w0 helicobacte
15	79	7.4	477	1	TFB1_SCHPO	O13745 schizosacch
16	79	7.4	510	1	CBP1_ORYSA	P37890 oryza sativ
17	78.5	7.4	280	1	AROE_RACSU	P54374 bacillus su
18	78.5	7.4	917	1	DML3_ARATH	O49498 arabidopsis
19	78.5	7.4	1262	1	TPP2_MOUSE	Q64514 mus musculus
20	78.5	7.4	1828	1	MYSA_RAT	Q9QYF3 rattus norv
21	78	7.3	337	1	HAIR_DROME	P14003 drosophila
22	78	7.3	887	1	ITH3_RAT	Q63416 rattus norv
23	78	7.3	1853	1	MYSA_MOUSE	Q99104 mus musculu
24	78	7.3	1855	1	MYSA_HUMAN	Q9Y411 homo sapien
25	77	7.2	729	1	YP65_CABEL	O09214 caenorhabdi
26	76.5	7.2	524	1	HY11_BRAJA	P59385 bradyrhizob
27	76.5	7.2	1025	1	PO21_NASVI	Q03278 nasonia vit
28	76	7.1	543	1	OPPA_ECOLI	P23843 escherichia
29	76	7.1	1650	1	VIT6_CABEL	P18948 caenorhabdi
30	76	7.1	2145	1	US20_CABEL	Q9U290 caenorhabdi
31	75.5	7.1	580	1	TRE2_WCTTU	Q10769 mycobacteri
32	75.5	7.1	2318	1	NTC3_MOUSE	Q61982 mus musculu
33	75	7.1	1694	1	SN_MOUSE	Q62230 mus musculu

```
RESULT 2
NP77_XENLA STANDARD; PRT; 185 AA.
AC P55869;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Putative secreted protein NP77 precursor.
GN NP77.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Cement gland;
RA Aberger F., Schueren C., Lepperdinger G., Richter K., Grunz H.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN CEMENT GLAND
CC (POTENTIAL).
CC -1- SIMILARITY: HIGH, TO XENOPUS XAG.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U82110; AAB49974.1; -
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 185 AA; 20442 MW; AE3807C926044509 CRC64;

Query Match 41.2%; Score 437.5; DB 1; Length 185;
Best Local Similarity 53.5%; Pred. No. 9.1e-34;
Matches 84; Conservative 26; Mismatches 46; Indels 1; Gaps 1;

Qy 51 ARDTTVKPGAKDKTSRPKLPQLTSLRGWDQLTWTQTYEALYKSTNSKPLMIHHL 110
Db 29 AADTNGAKSEPAFVTKLTKLDRGWGEDIWAQTYEGLAKARENKPLMVIHLE 88

Qy 111 ECPHSQALKVFAENKEIQKLA-EQFVLLNLVYETTDKHLSPDQYVPRIMFVDPSTLTV 169
Db 89 DCFYSIALKAFVADKWAQKLAQEDFIMNLVHPVADENQSPDGHVYVPGKIFIDPSLTV 148

Qy 170 ADITGRYSNRLYAVEPADTALLDNNKALKLKTTEL 206
Db 149 SDLKGRYGNKLYAYDADDIPELITNMKKAKSFLKTTEL 185

RESULT 3
TL19 MOUSE
ID TL19 MOUSE STANDARD; PRT; 170 AA.
AC Q9CQU0;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Thiorodexin-like protein p19 precursor (Endoplasmic reticulum protein
DE ERp19).
GN TL19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Embryo, and Kidney;
RC STRAIN=C57BL/6J; Thiorodexin; 1.
```

FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 170 THIOREDOXIN-LIKE PROTEIN P19.  
 FT DISULFID 64 67 REDOX-ACTIVE (POTENTIAL).  
 FT SITE 167 170 PREVENT SECRETION FROM ER (POTENTIAL).  
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 170 AA; 19048 MW; 5B91FC9BE12C5E44 CRC64;  
 Query Match 21.1%; Score 224.5; DB 1; Length 170;  
 Best Local Similarity 34.9%; Pred. No. 6.4e-14;  
 Matches 58; Conservative 25; Mismatches 58; Indels 25; Gaps 4;  
 QY 39 AFLIALVALSYLTARDTTVKPGAKKTKDSRPKLPQTLRGWGDQLIWTQTYEALYKSKT 98  
 DB 14 SFLLITSS-----DGR-----TGLGKGFQDHIHW-RTLEDGKKEAAA 50  
 QY 99 SNKPLMIHHLDECPHSQALKKVFANKEIQKLAQFVLLNL--VYETDKHLSPDGQV 156  
 DB 51 SGLPLMVLIIHSCWCAKALKPKFAESTEISLSHFVNVNLEDEEPRDEDFSPDGGYI 110  
 QY 157 PRIMVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLL 202  
 DB 111 PRILFDPSGKVRPIINESGNPSYKVFVSAEQVVGKKEAQL 156

## RESULT 4

TL19 HUMAN STANDARD; PRT; 172 AA.  
 ID TL19 HUMAN  
 AC O95881; Q96H50;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Thioredoxin-like protein p19 precursor (Endoplasmic reticulum protein ERp19).  
 GN TLP19.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mei G., Yu W., Gibbs R.A.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Liu F., Rong Y., Zeng L., Qi X., Han Z.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Colon, Kidney, and Ovary;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshitoki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -!- SIMILARITY: Contains 1 thioredoxin domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; AF131758; AAD20035.1; -  
 DR EMBL; AF543416; AAN34781.1; -  
 DR EMBL; BC001493; AAH01493.1; -  
 DR EMBL; BC008953; AAH08953.1; -  
 DR EMBL; BC008913; AAH08913.1; -  
 DR InterPro; IPR006662; Thior.  
 DR InterPro; IPR006663; Thior.  
 DR PROSITE; PS00194; Thior.  
 KW Endoplasmic reticulum; Redox-active center; Signal.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 172 THIOREDOXIN-LIKE PROTEIN P19.  
 FT DISULFID 66 69 REDOX-ACTIVE (POTENTIAL).  
 FT SITE 169 172 PREVENT SECRETION FROM ER (POTENTIAL).  
 FT CONFLICT 102 102 D -> H (IN REF. 3; AAH08913).  
 SQ SEQUENCE 172 AA; 19206 MW; 3092E9515A7C4094 CRC64;

Query Match 20.9%; Score 222; DB 1; Length 172;  
 Best Local Similarity 34.2%; Pred. No. 1.1e-13;  
 Matches 54; Conservative 26; Mismatches 56; Indels 22; Gaps 3;  
 QY 66 DSRPKLPOT-----LSRGWGDQLIWTQTYEALYKSKTSNPLMI 106  
 DB 2 ETRPRLGATLLGFSFLLLVSSDCHNGLGKGFQDHIHW-RTLEDGKKEAASGLPLMVI 60  
 QY 107 HLDCEPHSQALKKVFANKEIQKLAQFVLLNL--VYETDKHLSPDGQVPRIMFVDP 164  
 DB 61 IHKSWGCAKALKPKFAESTEISLSHFVNVNLEDEEPRDEDFSPDGGYIPRILFDLP 120  
 QY 165 SLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLL 202  
 DB 121 SGKVHEIINENGNSPKYKVFVSAEQVVGKKEAQL 158

## RESULT 5

YM51 YEAST STANDARD; PRT; 458 AA.  
 ID YM51 YEAST  
 AC P42933;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical 52.2 kDa protein in SGS1-MRPL24 intergenic region.  
 GN YMR191W OR YMR646.03.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288C / AB972;  
 RX PubMed=9169872;  
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,  
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,  
 RA Jagels K., Lyle G., Moule S., Odell C., Pearson D., Rajandream M.A.,  
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrall B.G.;  
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII."  
 RL Nature 387:90-93 (1997).  
 RN [2]  
 RP SEQUENCE OF 1-249 FROM N.A.  
 RC STRAIN=W303;  
 RX MEDLINE=95059068; PubMed=7969174;  
 RA Gangloff S., McDonald J.P., Bendixen C., Arthur L., Rothstein R.;  
 RT "The yeast type I topoisomerase Top3 interacts with Sgs1, a DNA helicase homolog: a potential eukaryotic reverse gyrase."

```

RL Mol. Cell. Biol. 14:8391-8398(1994).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z47815; CAA87812.1; -.
DR EMBL; U22341; AAB60288.1; -.
DR PIR; S50919; S50919.
DR SGD; S0004803; YMR191W.
KW Hypothetical protein.
FT CONFLICT 128 128 N -> Y (IN REF. 2).
FT CONFLICT 132 135 FVTW -> LALG (IN REF. 2).
SQ SEQUENCE 458 AA; 52183 MW; C31107D7B28DAE33 CRC64;

Query Match      8.2%; Score 87.5; DB 1; Length 458;
Best Local Similarity 20.1%; Pred. No. 1.4; Indels 109; Gaps 13;
Matches 55; Conservative 35; Mismatches 74;

QY 15 PSRLTGG-----RWKRSVAMEKIPVSAPFLILVALS----- 47
DB 82 PTPNMAVGGNWSWMLRMSRVHLRQITKSLDRLTILSLHGNFSHQYNRNFVTWKSLE 141

QY 48 -----YTLARTTVKPGAKKDTK-----DSRPKLQTLRSG-----W-----GD 81
DB 142 ASTAFRRASGLTWSPLTRRGIRDFHPRPVPNVSKFASFPVPKGPRLFTNNMTTSK 201

QY 82 QLIWTQTYEALYK---SKTSNKPLMI-----IHHLDECPSHQ----- 116
DB 202 RLLGQRAYTSISIKFTQEAANNMTISURCFNSLGGNLQCHSNSCKAYONASNVTSKOD 261

QY 117 -----ALKKV-----PAENKEIQKLAEQFVLNLVYETTDKHLSPGQYV----- 156
DB 262 HVQPVALKLSQKSDINIRNLELPKIMK--TQNEVDVETSAYYMEKPGSVIETISFN 319

QY 157 -----PRIMVDPSLTVRADITGRYSNRLYAYE 184
DB 320 NGTFSAPLSLDPSSL--ADLDEMIRN--YKYE 348

```

## RESULT 6

```

MISA_CHICK
ID MYSA_CHICK STANDARD; PRT; 1829 AA.
AC Q02440;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin Va (Myosin 5A) (Dilute myosin heavy chain, non-muscle) (Myosin
DE heavy chain P190) (Myosin-V).
GN MYO5A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=33012002; PubMed=1381040;
RA Sanders G., Lichte B., Meyer H.E., Kilmann M.W.;
RT "cDNA encoding the chicken ortholog of the mouse dilute gene product.
RT Sequence comparison reveals a myosin I subfamily with conserved C-
RT terminal domains."
RL FEBS Lett. 311:295-298 (1992).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1154-1163.
RC TISSUE=Brain;
RX MEDLINE=93107155; PubMed=1469047;
RA Espreafico E.M., Cheney R.E., Matteoli M., Nascimento A.A.,

```

```

RA de Camilli P.V., Larson R.E., Mooseker M.S.;
RT "Primary structure and cellular localization of chicken brain
RT myosin-V (p190), an unconventional myosin with calmodulin light
RT chains.";
RL J. Cell Biol. 119:1541-1557(1992).
CC -!- FUNCTION: PROCESSIVE ACTIN-BASED MOTOR THAT CAN MOVE IN LARGE
CC STEPS APPROXIMATING THE 36-NM PSEUDO-REPEAT OF THE ACTIN FILAMENT.
CC MAY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, IT MAY
CC BE REQUIRED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRITE
CC FORMATION (BY SIMILARITY).
CC -!- SUBUNIT: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE
CC CALMODULIN OR MYOSIN LIGHT CHAINS.
CC -!- SUBCELLULAR LOCATION: GOLGI-DERIVED CYTOPLASMIC MEMBRANES
CC (POTENTIAL).
CC -!- TISSUE SPECIFICITY: NEURONAL AND NONNEURONAL CELLS OF THE BRAIN.
CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -!- SIMILARITY: Contains 1 dilute domain.
CC -!- SIMILARITY: Contains 6 IQ domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X67251; CAA47673.1; -.
DR EMBL; Z11718; CAA77782.1; -.
DR PIR; S19188; S19188.
DR HSSP; P10587; 1BR2.
DR InterPro; IPR002710; DIL.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; myosin_head.
DR Pfam; PF01843; DIL; 1.
DR Pfam; PF00612; IQ; 6.
DR Pfam; PF00063; myosin_head; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD003376; DIL; 1.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 6.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 6.
KW Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
KW Coiled coil; Phosphorylation.
FT DOMAIN 1 766 MYOSIN HEAD-LIKE.
FT DOMAIN 767 789 IQ 1.
FT DOMAIN 790 814 IQ 2.
FT DOMAIN 815 837 IQ 3.
FT DOMAIN 838 862 IQ 4.
FT DOMAIN 863 887 IQ 5.
FT DOMAIN 888 915 IQ 6.
FT DOMAIN 916 1239 COILED COIL (POTENTIAL).
FT DOMAIN 1315 1419 COILED COIL (POTENTIAL).
FT DOMAIN 1661 1766 DILUTE.
FT NP_BIND 163 170 ATP (BY SIMILARITY).
FT DOMAIN 644 666 ACTIN-BINDING (POTENTIAL).
FT MOD_RES 1734 1734 PHOSPHORYLATION (POTENTIAL).
FT CONFLICT 1142 1142 E -> EQ (IN REF. 2).
SQ SEQUENCE 1829 AA; 212381 MW; 0538B278DFC09F6E CRC64;

Query Match      8.0%; Score 85.5; DB 1; Length 1829;
Best Local Similarity 28.1%; Pred. No. 13;
Matches 27; Conservative 21; Mismatches 41; Indels 7; Gaps 3;

QY 63 DTKDSRPKLPQTLRSRGWQDLWTQTYEALY-KSKTSNKPLMIHHLDECPSH--SOALK 119
DB 507 DLLDECKPKPGSDDTWAQKLYNTHLNKCALFEKPRLSNKAFLIKHFADKVEQCEGLE 566

QY 120 K-----VFAENKEIQKLAEQFVLNLVYETTDKHLSP 151
DB 567 KNKDTVYEEQIKVLKSSKKFKLLPELFQDEKAISP 602

```

## RESULT 7

REF1 YEAST  
ID REF1 YEAST STANDARD; PRT; 811 AA.  
AC P48743;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE RFX-like DNA-binding protein RFX1.  
GN RFX1 OR CRT1 OR YLR176C OR L9470.18.  
OS Saccharomyces cerevisiae (Baker's Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288c / AB972;  
RX MEDLINE=97313267; PubMed=9169871;  
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansoerge W.,  
RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,  
RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,  
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,  
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,  
RA Mueller-Auer S., Newtlich U., Obermaier B., Piravandi E., Pohl T.M.,  
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,  
RA Scharfe M., Scherrens B., Scholler P., Schwager C., Schwarz S.,  
RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,  
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,  
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohelsel J.D.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";  
RL Nature 387:87-90 (1997).  
CC -!- SIMILARITY: BELONGS TO THE RFX FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
CC EMBL; U17246; AAB67470.1; -  
CC SGD; S0004166; RFX1.  
CC GO; GO:0005737; C:nucleus; IDA.  
CC GO; GO:0005634; C:nucleus; IDA.  
CC GO; GO:0016566; F:specific transcriptional repressor activity; IDA.  
CC GO; GO:000122; P:negative regulation of transcription from P. .; IDA.  
CC InterPro; IPR003150; RFX\_DNA\_binding.  
CC Pfam; PF02257; RFX\_DNA\_binding; 1.  
CC DNA-binding.  
CC  
CC SEQUENCE 811 AA; 90583 MW; 116A88B7DDE4FBF0 CRC64;

Query Match 7.9%; Score 84; DB 1; Length 811;  
Best Local Similarity 25.7%; Pred. No. 6.4;  
Matches 47; Conservative 29; Mismatches 67; Indels 40; Gaps 8;  
OY 8 LSGSOP-----HPSRLTQGR-----WVRKSRVAMEKIPVSAFLLVALSYTLAR 52  
DB 129 LIGSGPGSHKSPPTTPQAPQATQRPATQSVYPASISLRNSASPLSPKSEETLNN 188  
OY 53 D--TTVK-----PGAKDQTKSRPKLPQTLSRGWDQLTIWTQTYEALYKSTSNKP 102  
DB 189 NPPTAAKRTNTFPSPISPTTKQKTSQEKRISSSRNTQETIAKQIAEN--NKSXTIEY 246  
OY 103 LMTHH-----LDECHPSOALKKVFANKEIQKLAQFVLNVLNLTTHKHSIDGQY 155  
DB 247 AQIVKHAEIKVLKSMDSQNTSKAALQALQNRERER--QVFALLMLMKNSQHS----Y 300  
OY 156 VPR 158  
DB 301 VPR 303

## RESULT 8

YD67 SCHPO  
ID YD67 SCHPO STANDARD; PRT; 217 AA.  
AC Q10319;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein C17G8.07 in chromosome I.  
GN SPAC17G8.07.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Gailfaut A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880 (2002).  
CC -!- SIMILARITY: TO HUMAN AF9 AND ENL AND YEAST TRANSCRIPTION  
CC -!- SIMILARITY: STRONG. TO YEAST YNL107W.

This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
CC EMBL; Z69795; CAA93690.1; -  
CC PIR; T37859; T37859.  
CC GenDB SPombe; SPAC17G8.07; -  
CC InterPro; IPR005033; YEATS.  
CC Pfam; PF03366; YEATS; 1.  
CC Hypothetical protein.  
CC SEQUENCE 217 AA; 24946 MW; A274C2AFB0620D7F CRC64;

Query Match 7.9%; Score 83.5; DB 1; Length 217;  
Best Local Similarity 20.6%; Pred. No. 1.3;  
Matches 42; Conservative 33; Mismatches 80; Indels 49; Gaps 8;  
OY 14 HPSRLTQGR-----RWVRKSRVAMEKIPVSAFLLVALSYTLARDTTVKPGAKDQTKD 66  
DB 39 HTWRFIFVEGVGDGDISKWVRK-----VVFKL-----HDTYNNP-----TRTIE 76  
OY 67 SRPKLPQTLSRGWDQLTIWTQTYEALYKSTSNKPLMI IHLDCECHPSOALKKVFANKEI 126

```

Db 77 SPPF--EVIEGTGGEFDMVRIF-----FAPEAHEKALTFFHLLKHPYGRPMEMKASGG 130
Qy 127 EIQKLARQFVLLNLVYETTKHLSPP-----DQGVPRIMFVDPSTLTVRADITGRYSNRLYA 182
Db 131 LVSEVQVEEIVFNEPFYTYKLLSQNPIDGDI-----GLAVESEPHDPFSSQOLEQ 180
Qy 183 YEPADTALLDNNMKKALKLKTSL 206
Db 181 DEADKLDFAIQEVKTIEMTKQQV 204

```

## RESULT 9

```

HSL1 SCHPO
ID HSK1 SCHPO STANDARD; PRT; 507 AA.
AC P50582; 094678;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell cycle protein kinase hsk1 (EC 2.7.1.-).
GN HSK1 OR SPBC776.12C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=JY2;
RX MEDLINE=95347336; PubMed=7621824;
RA Masai H., Miyake T., Arai K.-I.;
RT "hsk1", a Schizosaccharomycetes pombe gene related to Saccharomycetes
RT cerevisiae CDC7, is required for chromosomal replication.;
RL EMBL J. 14:3094-3104(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scourto J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weijtens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Gaffard F., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Uesary D., Barrell B.G., Nurse P.;
RT "the genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: REQUIRED FOR CHROMOSOMAL REPLICATION.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=PF050582-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=PF050582-2; Sequence=VSP_004863;
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC7
CC SUBFAMILY.

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; D50493; BAA09087.1; -
CC DR EMBL; AL035263; CA22885.1; -
CC DR EMBL; AL035263; CAB38417.1; -
CC DR PIR; S56143; S56143.
CC DR PIR; T40683; T40683.
CC DR GeneDB_Spombe; SPBC776.12C; -
CC DR InterPro; IPR000719; Prot_kinase.
CC DR InterPro; IPR002290; Ser_thr_kinase.
CC DR Pfam; PF00069; pkinase; 1.
CC DR ProDom; PD000001; Prot_kinase; 2.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC KW Cell cycle; Cell division; Serine/threonine-protein kinase;
CC Transferase; ATP-binding; Alternative splicing.
CC FT DOMAIN 68 433 PROTEIN_KINASE.
CC FT NP_BIND 74 82 ATP (BY SIMILARITY).
CC FT BINDING 129 129 ATP (BY SIMILARITY).
CC FT ACT_SITE 216 216 BY SIMILARITY.
CC FT VARSPPLIC 92 119 Missing (in isoform Short).
CC FT VSP 004863.
CC SQ SEQUENCE 507 AA; 58407 MW; 04970E58218441EE CRC64;
Query Match 7.8%; Score 83; DB 1; Length 507;
Best Local Similarity 22.4%; Pred. No. 4.3;
Matches 28; Conservative 24; Mismatches 55; Indels 18; Gaps 5;
Qy 83 LIWDTVEEALYKSTNKP-----LMIHLDSPHSQALKVFAENKEIQKLAEQFVLL 138
Db 380 ILWASGCSASIKYKLRHPSQERCLDFLEKCLDCKRISAE-----EALDHDFLYL 435
Qy 139 -NLVYETTKHLSPPDQGVPRIMFVDPSTLTVRADITGRYSNRLYA---EPADTALLDN 194
Db 436 DNLAYEKDDDTAFDINS-----FGTSPFKDLDLTAHLHLDLDFKEQEBETDEPTSLSK 489
Qy 195 MKAL 199
Db 490 RKRSI 494
RESULT 10
OCRL_HUMAN
ID OCRL_HUMAN STANDARD; PRT; 901 AA.
AC Q01968; Q08000; Q15684; Q15774; Q9JUG5; Q9UMA5;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inositol polyphosphate 5-phosphatase OCRL-1 (EC 3.1.3.36) (Lowe's
DE oculocerebrorenal syndrome protein).
GN OCRL OR OCRL1 OR INPP5F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Kidney;
RX MEDLINE=92334430; PubMed=1321346;
RA Attree O., Olivos I.M., Okabe I., Bailey L.C., Nelson D.L.,
RA Lewis R.A., McInnes R.R., Nussbaum R.L.;
RT "The Lowe's oculocerebrorenal syndrome gene encodes a protein highly
RL homologous to inositol polyphosphate-5-phosphatase.";
RN [2]

```





RT	counseling.";
RL	Hum. Mutat. 16:157-165 (2000).
RN	[13]
RP	VARIANTS LS PRO-337 AND GLY-372.
RX	MEDLINE=20232168; PubMed=10767176;
RA	Roschinger W., Muntau A.C., Rudolph G., Roscher A.A.,
RA	Kammerer S.;
RA	"Carrier assessment in families with Lowe oculocerebrorenal syndrome:
RT	novel mutations in the OCR1L1 gene and correlation of direct DNA
RT	diagnosis with ocular examination.";
RL	Mol. Genet. Metab. 69:213-222 (2000).
CC	-1- FUNCTION: Converts phosphatidylinositol 4,5-bisphosphate to
CC	phosphatidylinositol 4-phosphate. Also converts inositol 1,4,5-
CC	trisphosphate to inositol 1,4-bisphosphate and inositol 1,3,4,5-
CC	tetrakisphosphate to inositol 1,3,4-trisphosphate. May function in
CC	lysosomal membrane trafficking by regulating the specific pool of
CC	phosphatidylinositol 4,5-bisphosphate that is associated with
CC	lysosomes.
CC	-1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4',5'-
CC	bisphosphate + H(2)O = 1-phosphatidyl-1D-myo-inositol 4-phosphate
CC	+ phosphate.
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event-Alternative splicing; Named isoforms=2;
CC	Names=A;
CC	Isoid=Q01968-1; Sequence=Displayed;
CC	Name=B;
CC	Isoid=Q01968-2; Sequence=VSP 002681;
CC	-1- TISSUE SPECIFICITY: BRAIN, SKELETAL MUSCLE, HEART, KIDNEY, LUNG,
CC	PLACENTA, AND FIBROBLASTS.
CC	-1- DISEASE: DEFECTS IN OCR1L1 ARE THE CAUSE OF LOWE'S OCULOCEREBRORENAL
CC	SYNDROME, A DISEASE CHARACTERIZED BY HYDROPHALMIA, CATARACT,
CC	MENTAL RETARDATION, VITAMIN D-RESISTANT RICKETS, AMINOACIDURIA,
CC	AND REDUCED AMMONIA PRODUCTION BY THE KIDNEY.
CC	-1- SIMILARITY: BELONGS TO THE INOSITOL-1,4,5-TRISPHOSPHATE 5-
CC	PHOSPHATASE TYPE II FAMILY.
CC	-1- SIMILARITY: Contains 1 Rho-GAP domain.
CC	-1- DATABASE: NAME=Lowe Syndrome mutation database;
CC	WWW="http://research.nhgri.nih.gov/lowe/".
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collabora-
CC	tion between the Swiss Institute of Bioinformatics and the EMBL Outstat-
CC	the European Bioinformatics Institute. There are no restrictions on
CC	use by non-profit institutions as long as its content is in no
CC	modified and this statement is not removed. Usage by and for comm-
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/anno">http://www.isb-sib.ch/anno</a> )
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .
CC	-----
DR	EMBL; M88162; AAA59964.1; ALT_INIT.
DR	EMBL; U57627; AAB03839.2; --
DR	EMBL; AL022162; CAA18150.1; --
DR	EMBL; AL022162; CAA18151.1; --
DR	EMBL; Z73496; CAA97842.1; --
DR	EMBL; S62085; AAB26926.1; --
DR	PIR; S29069; S29069.
DR	Genew; HGNC:8108; OCR1L1.
DR	MTM; 309000; --
DR	GO; GO:0005795; C:Golgi stack; TAS.
DR	GO; GO:0005798; C:Golgi vesicle; TAS.
DR	GO; GO:0004439; F:phosphatidylinositol-bisphosphatase activity; TAS.
DR	GO; GO:0006629; P:lipid metabolism; TAS.
DR	InterPro; IPR005135; Exo_endo_phos.
DR	InterPro; IPR000300; IPPC
DR	InterPro; IPR000198; RhoGAP.
DR	Pfam; PF03372; Exo_endo_phos; 1.
DR	Pfam; PF00620; RhoGAP; 1.
DR	SMART; SM00128; IPPC; 1.
DR	SMART; SM00324; RhoGAP; 1.
DR	PROSITE; PS00338; RHO_GAP; 1.
KW	Hydrolase; Alternative splicing; Disease mutation.
FT	DOMAIN 721 901
FT	VARSPPLIC 707 714
FT	-----
FT	VARIANT 337 337
FT	R -> P (IN LOWE SYNDROME).





```
CC EMBL; AE001480; AAD06035.1; -
DR PIR; G71929; G71929.
DR HSP; P06616; IEQA.
DR HAMAP; MF 00367; -; 1.
DR InterPro; IPR005662; Era.
DR InterPro; IPR004087; KH dom.
DR InterPro; IPR004044; KH_TYPE 2.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00013; KH; 1.
DR TIGRFAMs; TIGR00436; era; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS0823; KH TYPE 2; 1.
KW GTP-binding; RNA-binding; Complete proteome.
FT NP_BIND 12 19 GTP (POTENTIAL).
FT NP_BIND 64 68 GTP (POTENTIAL).
FT NP_BIND 122 125 GTP (POTENTIAL).
FT DOMAIN 204 280 KH TYPE-2.
SQ SEQUENCE 301 AA; 34485 MW; F668C7730892EDBF CRC64;

Query Match 7.58; Score 79.5; DB 1; Length 301;
Best Local Similarity 27.8%; Pred. No. 4.7;
Matches 25; Conservative 13; Mismatches 33; Indels 19; Gaps 4;

QY 89 YEALYKSKTSNKP-LMIHHLDECPHSQALKVFAENKEIQKLAEOFLV-----137
Db 106 YEBFL---SUCQPHILAKSIDATHKQVLQKL-----QYQKYSQFLALVPLSAKKSQ 158
QY 138 -LNLVYETTDKHLSPDQGYVPRIMFVDPDL 166
Db 159 NLNALLELCISKHLSPSAWLFEKDLMSDEKM 188

RESULT 15
TFBI_SCHPO STANDARD; PRT; 477 AA.
ID Q13745;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative RNA polymerase II transcription factor TFIIF subunit 1.
GN SPAC16E8.11C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brookes K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Gaffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
```

```
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Component of the core-TFIIF basal transcription factor
CC (potential).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 2 BSD domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z98529; CAB11039.1; -.
DR PIR; T37791; T37791.
DR GeneDB SPombe; SPAC16E8.11c; -.
DR InterPro; IPR005607; BSD.
DR Pfam; PF03909; BSD; 2.
DR PROSITE; PS0858; BSD; 2.
KW Hypothetical protein; Transcription regulation; Nuclear protein;
KW Repeat.
FT DOMAIN 60 113 BSD 1.
FT DOMAIN 134 185 BSD 2.
SQ SEQUENCE 477 AA; 54558 MW; E21CCF7EC370C34C CRC64;

Query Match 7.4%; Score 79; DB 1; Length 477;
Best Local Similarity 26.3%; Pred. No. 9.5;
Matches 36; Conservative 21; Mismatches 42; Indels 38; Gaps 8;

QY 87 QTYEALYKSKTSNKP-----LMIHHLDEC-----PHS--OALK-----KYPAN 125
Db 85 QTFKEAVMKHLSNEQFWSTRLHLRAHAVERSQQRGPNVLSITKPTVDNMKVS LTG 144
QY 126 KEIQKLAEOFLVNLVYETTDKHLSP--DQGVYPRIMFVDPDLTVRADITGRYSNRLYAY 183
Db 145 QQIHDHFEQHPPLRKVY---DKHVPPLAGEFWSRFFLSKLCCKLKG D-----RITPM 194
QY 184 EPADTALLLDNMKKALK 200
Db 195 DPSPD-----DINDKYLK 206
```

Search completed: November 26, 2003, 15:55:04  
Job time : 20 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2003, 15:52:23 ; Search time 35 Seconds  
(without alignments)  
1518.824 Million cell updates/sec

Title: US-09-674-266A-181  
Perfect score: 1063  
Sequence: 1 RLSCAGTSLGSGPHPSRLT.....DTALLDNKKALKLKTTEL 206

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	899	84.6	175	4	O95994
2	828	77.9	175	11	O88312
3	555	52.2	165	11	Q8R3W7
4	555	52.2	166	4	Q8TD06
5	550	51.7	165	11	Q8BW95
6	548	51.6	159	13	Q90Y05
7	447	42.1	185	13	O42251
8	227	21.4	172	4	Q96H50
9	224.5	21.1	170	11	Q9CQU0
10	222	20.9	172	4	O95881
11	199	18.7	186	5	Q9NA78
12	165	15.5	257	5	Q9NS57
13	119	11.2	150	17	O27777
14	113.5	10.7	357	16	Q8EXX9
15	89	8.4	950	11	Q924S5
16	88.5	8.3	737	2	Q9AF04

17	87.5	8.2	824	16	Q8FI25
18	87	8.2	348	16	Q926X3
19	85	8.0	1620	5	Q8IIV3
20	84.5	7.9	378	16	Q8XIU3
21	84.5	7.9	1151	16	Q929J2
22	84	7.9	435	5	Q9BJK8
23	84	7.9	463	5	O18141
24	83.5	7.9	268	10	Q8L7Y4
25	83.5	7.9	595	10	Q8L5D2
26	83.5	7.9	918	10	Q9CA88
27	83.5	7.9	1011	5	Q9UPP6
28	83.5	7.9	1409	5	Q9V3A7
29	83.5	7.9	1409	5	Q9V6I2
30	83	7.8	786	4	Q9H747
31	83	7.8	976	5	Q9U158
32	82.5	7.8	788	16	O67557
33	82	7.7	242	5	Q8I428
34	81.5	7.7	649	10	Q9CSB1
35	81.5	7.7	926	16	Q8PF46
36	81.5	7.7	1158	3	Q9UTR5
37	81.5	7.7	1472	5	Q8ILC8
38	81.5	7.7	1721	5	Q8SSQ0
39	81	7.6	601	5	Q9S598
40	81	7.6	610	5	Q9XVM2
41	80.5	7.6	802	4	Q8TB22
42	80.5	7.6	875	12	Q9QG39
43	80	7.5	154	16	Q9PCE7
44	80	7.5	259	10	Q9M9H0
45	80	7.5	563	5	Q8I0B7

## ALIGNMENTS

## RESULT 1

O95994 ID O95994 PRELIMINARY; PRT; 175 AA.  
 AC O95994;  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE Secreted CEMENT gland protein XAG-2 homolog (Anterior GRADIENT 2  
 DE (XENEPUS LAEVIS) homolog) (XAG-2 homolog long protein).  
 GN HAG-2/R OR HAG-2/C OR HPC8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RC TISSUE=Breast;  
 RX MEDLINE=99009231; PubMed=9790916;  
 RA Thompson D.A., Weigel R.J.;  
 RT "HAG-2, the human homologue of the Xenopus laevis cement gland gene  
 RT XAG-2, is coexpressed with estrogen receptor in breast cancer cell  
 RT lines.";  
 RL Biochem. Biophys. Res. Commun. 251:111-116(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast;  
 RX MEDLINE=99009231; PubMed=9790916;  
 RA Thompson D.A., Weigel R.J.;  
 RT "HAG-2, the human homologue of the Xenopus laevis cement gland gene  
 RT XAG-2, is coexpressed with estrogen receptor in breast cancer cell  
 RT lines.";  
 RL Biochem. Biophys. Res. Commun. 251:111-116(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RX Strausberg R.;  
 RA Strausberg R.;  
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RX Zhang J.S., Smith D.I.;  
 RA Zhang J.S., Smith D.I.;  
 RT "Human homolog of XAG is differentially expressed in tumors.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RX Zhang J.S., Smith D.I.;  
 RA Zhang J.S., Smith D.I.;  
 RT "Identified of human homolog of XAG-2 over-expressed in tumors.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF038451; AAC82614.1; -.



```

Q8TD06;
01-JUN-2002 (Tremblrel. 21, Created)
01-JUN-2002 (Tremblrel. 21, Last sequence update)
01-JUN-2002 (Tremblrel. 21, Last annotation update)
Anterior gradient protein 3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
Adam P.J., Boyd R., Fletcher G.C., Tyson K., Terrett J.;
"Proteomic Characterization of Breast Cancer Cell Membranes.";
Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AY069977; AAL55402.1; -.
SEQUENCE 166 AA; 19171 MW; B1A4804B47705D65 CRC64;

Query Match      52.2%; Score 555; DB 4; Length 166;
Best Local Similarity 64.7%; Pred. No. 1.2e-46;
Matches 108; Conservative 28; Mismatches 19; Indels 12; Gaps 4;

QY 41 LLLVALSYTLARDTTVKPKAKKDTKDSRPKLPQTLSRGWGDQIWTQTYEALYKSKTSN 100
DB 11 LLLTVSSNLA--IAIK-----KEKRP--PQTLSRGWGDITWVQTYEGLFLYAKSK 59

QY 101 KPLMIHHLDECPHQALKKVFAENKEIOKLAE-QFVLNLVYETDKHLSPDGQVVPRI 159
DB 60 KPLMVIHLEDCQYQALKKVFAENKEIQEAMQNFIMLNLMHETDKNLSPDGQVVPRI 119

QY 160 MFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206
DB 120 MFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLRIQSEL 166

RESULT 5
Q8BW95 PRELIMINARY; PRT; 165 AA.
AC Q8BW95;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE weakly similar to secreted CEMENT gland protein XAG-2 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAINE=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcription repertoire based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK053177; BAC35297.1; -.
SEQUENCE 165 AA; 19139 MW; 243BC7D9A27A173D CRC64;

Query Match      51.7%; Score 550; DB 11; Length 165;
Best Local Similarity 63.5%; Pred. No. 3.8e-46;
Matches 106; Conservative 28; Mismatches 21; Indels 12; Gaps 4;

QY 41 LLLVALSYTLARDTTVKPKAKKDTKDSRPKLPQTLSRGWGDQIWTQTYEALYKSKTSN 100
DB 10 LLLTVSSNLA--IAIK-----KEKRP--PQTLSRGWGDITWVQTYEGLFLYAKSKN 58

QY 101 KPLMIHHLDECPHQALKKVFAENKEIOKLAE-QFVLNLVYETDKHLSPDGQVVPRI 159
DB 59 KPLMVIHLEDCQYQALKKVFAENKEIQEAMQNFIMLNLMHETDKNLSPDGQVVPRI 118

QY 160 MFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206
DB 119 MFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLRIQSEL 165

```

```

RESULT 6
Q90Y05 PRELIMINARY; PRT; 159 AA.
ID Q90Y05;
AC Q90Y05;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Cement gland-specific protein CGS
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=83355;
[1]
SEQUENCE FROM N.A.
Alexandrova E.M., Novoselov V.V., Zarskiy A.G.;
"Three novel genes expressed in the anterior part of the Xenopus
RT laevis embryo.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314056; AAL26844.1; -.
SEQUENCE 159 AA; 18275 MW; 738D6228483888EB CRC64;

Query Match      51.6%; Score 548; DB 13; Length 159;
Best Local Similarity 60.0%; Pred. No. 5.7e-46;
Matches 105; Conservative 26; Mismatches 28; Indels 16; Gaps 1;

QY 32 MEKIPVSFLLLVSYTLARDTTVKPKAKKDTKDSRPKLPQTLSRGWGDQIWTQTYEE 91
DB 1 METVLKSLFFLLVATSFYLAKE-----RKPTLSRGWGDNLFWQTYEE 44

QY 92 ALYKSKTSNKLMIHHLDECPHQALKKVFAENKEIOKLAE-QFVLNLVYETDKHLS 151
DB 45 GLFKAENKPELLLNHRNDCPHSQALKAFAEHQGIQKLAEFLLNVLVYDPTDKNLQ 104

QY 152 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206
DB 105 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 159

RESULT 7
O42251 PRELIMINARY; PRT; 185 AA.
ID O42251;
AC O42251;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE Cement gland-specific.
GN XAG-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=83355;
[1]
SEQUENCE FROM N.A.
TISSUE=Head;
RX MEDLINE=89324051; PubMed=2752418;
RA Sive H.L., Hattori K., Weintraub H.;
RT "Progressive determination during formation of the anteroposterior
RT axis in Xenopus laevis.";
RL Cell 58:171-180 (1989).
[2]
SEQUENCE FROM N.A.
TISSUE=Head;
RA Sive H.L., Mainstock D.H., Kennedy B.S.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF025474; AAB91968.1; -.
SEQUENCE 185 AA; 20498 MW; D6CDE02DEC3B857B CRC64;

Query Match      42.1%; Score 447; DB 13; Length 185;
Best Local Similarity 50.6%; Pred. No. 6.2e-36;

```

```
Matches 89; Conservative 26; Mismatches 49; Indels 12; Gaps 2;
QY 43 LVALLSYTLARDTTTKP-----GAKDTKDSRPKLPQTLSRGWGDLIWTQYEE 91
Db 10 LVLLCSVLGSAURKPKRQAGATNGAAKSEPAFVKTKGLKTLDRWGSDIEWAQTYEE 69
QY 92 ALYKSTSNKPLMIHLLDECPHSQALKKVFNAENKEIQKLA-EGVLLNLVYETDKHLS 150
Db 70 GLAKARENPLMVIHLEDCPYSLAKKFAVDKMAQKLAQEDFIMNLVHPVADENQS 129
QY 151 PDGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLTEL 206
Db 130 PDGHVPRVIFDPSLTVRSDLKGRYGNKLYAYDADDIPELITNMKKAFLKTEL 185

RESULT 8
ID Q96H50 PRELIMINARY; PRT; 172 AA.
AC Q96H50;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Ovary;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC008913; AA08913.1; -
DR InterPro; IPR006663; ThioRedox_dom2.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 172 AA; 19228 MW; 5C9DDA6D5A7C4BDF CRC64;

Query Match 21.4%; Score 227; DB 4; Length 172;
Best Local Similarity 34.8%; Pred. No. 2.5e-14;
Matches 55; Conservative 25; Mismatches 56; Indels 22; Gaps 3;

QY 66 DSRPKLPQT-----LSRGWGDLIWTQYEEALYKSTNKPMLII 106
Db 2 ETPRLGATCLLGFSEFLLLVSSDCHNLGKGFQDHIHW-RTLEDGKKEAAGLPMLVI 60

QY 107 HLLDECPHSQALKKVFNAENKEIQKLAEGVLLNLVYETTDKH--LSPDQYVPRIMFVDP 164
Db 61 IHKSWCCKALKPKFAESTEISELSHNFVWNLDEEPEPKHEDFSPDGGYIPRILFLDP 120

QY 165 SLTVRADITGRYSNRLYAYEPADTALLDNMKKALKL 202
Db 121 SGKVHPPIINENGPNPSYKYFVSAEQVVGQMKEAQERL 158

RESULT 9
Q9CQU0
ID Q9CQU0 PRELIMINARY; PRT; 170 AA.
AC Q9CQU0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE O610040B2IRK protein (RIKEN CDNA O610040B21 gene).
GN O610040B2IRK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Embryo, and Kidney;
RX MEDLINE=21085660; PubMed=11217851;
```

```
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Ozawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK003481; BAB22811.1; -
DR ENBL; AK002862; BAB22413.1; -
DR ENBL; BC006857; AA06857.1; -
DR MGD; MGI:1913323; O610040B2IRK.
DR InterPro; IPR00886; ER_target.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR PROSITE; PS00014; ER_TARGET; 1-
DR PROSITE; PS00194; THIOREDOXIN; 1.
SQ SEQUENCE 170 AA; 19048 MW; 5B91FC9BE12C5E44 CRC64;

Query Match 21.1%; Score 224.5; DB 11; Length 170;
Best Local Similarity 34.9%; Pred. No. 4.4e-14;
Matches 58; Conservative 25; Mismatches 58; Indels 25; Gaps 4;

QY 39 AFLLIVALSYTLARDTTTKPAGAKOTKDSRPKLPQTLSRGWGDLIWTQYEEALYKSKT 98
Db 14 SFLLITSS-----DGR-----TGLGKGFQDHIHW-RTLEDGKKEAAA 50

QY 99 SNKPLMIHLLDECPHSQALKKVFNAENKEIQKLAEGVLLNL--VYETTDKHLSPDQYV 156
Db 51 SGLPLMVIHKSCKGCKALKPKFAESTEISELSHNFVWNLDEEPEPRDEDFSPDGGYI 110

QY 157 PRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKL 202
Db 111 PRILFLDPGKVRPEINSGNPSYKYFVSAEQVVGQMKEAQERL 156

RESULT 10
Q95881
ID Q95881 PRELIMINARY; PRT; 172 AA.
AC Q95881;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Thioredoxin-like protein p19).
GN TLP19.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9620727; PubMed=8619474;
RA Andersson B., Wenland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
RT "A 'double adaptor' method for improved shotgun library
construction.";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
```







Db 315 VDNPIYLSMDGAALTGAESHEL--QDVLEETNIRKLYKALSLLKKE 359

Search completed: November 26, 2003, 15:55:52  
Job time : 37 secs

**THIS PAGE BLANK (USPTO)**